Attachment-I

No.	Score	E	Len		Accession	Organism
1419	119.5	7.7	10578	2	Q81SF5_CABEL	caenorhabdi
1420	119	7.7	413	2	Q99P0_ANTPE	antheraea p
1421	119	7.7	422	2	Q86CY9_HELAM	helicoverpa
1422	119	7.7	577	2	Q80Y42_MOUSE	mus musculu
1423	119	7.7	620	2	Q4S1C0_TETNG	tetraodon n
1424	119	7.7	675	2	Q4S5Q4_TETNG	tetraodon n
1425	119	7.7	880	2	Q7KPQ8_DROME	drosophila
1426	119	7.7	1187	2	Q589G5_CHICK	gallus gall
1427	119	7.7	1390	1	CONT_DROME	drosophila
1428	119	7.7	1390	2	Q5BI91_DROME	drosophila
1429	118.5	7.7	163	2	Q8K1H8_MOUSE	mus musculu
1430	118.5	7.7	269	2	Q5RC22_PONPY	pongo pygma
1431	118.5	7.7	285	2	Q5SNN8_BRARE	brachydanio
1432	118.5	7.7	302	2	Q5YU10_SHEEP	ovis aries
1433	118.5	7.7	342	2	P97635_RAT	rattus norv
1434	118.5	7.7	352	2	O76697_CABEL	caenorhabdi
1435	118.5	7.7	379	2	Q8BLX5_MOUSE	mus musculu
1436	118.5	7.7	397	2	Q8BFX8_MOUSE	n mus muscu
1437	118.5	7.7	467	1	SIGL7_HUMAN	homo sapien
1438	118.5	7.7	528	2	P91670_DROME	drosophila
1439	118.5	7.7	538	2	Q9NWQ7_HUMAN	homo sapien
1440	118.5	7.7	540	2	Q8N0Z9_HUMAN	homo sapien
1441	118.5	7.7	545	2	Q9VCT4_DROME	drosophila
1442	118.5	7.7	582	2	Q9SN25_BOVIN	bos taurus
1443	118.5	7.7	606	2	Q6IRH8_RAT	rattus norv
1444	118.5	7.7	697	1	SIG10_HUMAN	homo sapien
1445	118.5	7.7	717	2	Q7PUQ1_ANOGA	anopheles g
1446	118.5	7.7	912	1	ICAM5_RABIT	oryctolagus
1447	118.5	7.7	1187	2	Q8WR45_CABEL	caenorhabdi
1448	118.5	7.7	1195	2	Q5TU52_ANOGA	anopheles g
1449	118.5	7.7	1228	2	Q7QEI6_ANOGA	anopheles g
1450	118.5	7.7	1464	2	Q4SK55_TETNG	tetraodon n
1451	118.5	7.7	2646	2	Q48LN8_TETNG	tetraodon n
1452	118	7.7	175	2	Q4TGY2_TETNG	tetraodon n
1453	118	7.7	226	2	Q7PUJ2_ANOGA	anopheles g
1454	118	7.7	233	2	Q6PIW7_HUMAN	homo sapien
1455	118	7.7	253	1	O17858_CABEL	caenorhabdi
1456	118	7.7	270	2	Q8BTN8_MOUSE	mus musculu
1457	118	7.7	290	2	Q5TNT8_ANOGA	anopheles g
1458	118	7.7	321	2	Q8IWY0_HUMAN	homo sapien
1459	118	7.7	351	2	Q7QOP8_ANOGA	anopheles g
1460	118	7.7	381	2	Q4SDA6_TETNG	tetraodon n
1461	118	7.7	385	2	Q4SQV8_TETNG	tetraodon n
1462	118	7.7	421	2	Q9NT99_HUMAN	homo sapien
1463	118	7.7	430	2	Q5BF20_HUMAN	homo sapien
1464	118	7.7	553	2	Q8WXJ5_HUMAN	homo sapien
1465	118	7.7	620	2	SMP_COTJA	coturnix co
1466	118	7.7	626	2	Q90880_CHICK	gallus gall
1467	118	7.7	692	2	Q4RV46_TETNG	tetraodon n
1468	118	7.7	722	2	Q6GNB3_XENLA	xenopus lae
1469	118	7.7	769	2	Q8NI15_HUMAN	homo sapien
1470	118	7.7	806	1	CEK2_CHICK	gallus gall
1471	118	7.7	806	1	FGFR3_HUMAN	homo sapien
1472	118	7.7	814	2	Q91897_XENLA	xenopus lae
1473	118	7.7	838	2	Q8WXJ7_HUMAN	homo sapien
1474	118	7.7	847	1	FSTL5_HUMAN	homo sapien
1475	118	7.7	879	2	Q55FL9_HUMAN	homo sapien
1476	118	7.7	924	1	ICAM5_HUMAN	homo sapien
1477	118	7.7	1203	2	O4SRR2_TETNG	tetraodon n
1478	118	7.7	1415	2	Q94155_CABEL	caenorhabdi
1479	118	7.7	163	2	Q9NVJ5_HUMAN	homo sapien
1480	118	7.7	391	2	Q59EJ9_HUMAN	homo sapien
1481	117.5	7.6	398	2	Q9Y640_HUMAN	homo sapien
1482	117.5	7.6	403	1	RAGE_MOUSE	mus musculu
1483	117.5	7.6	467	2	Q91VT9_MOUSE	mus musculu
1484	117.5	7.6	467	2	Q8C6F2_MOUSE	mus musculu
1485	117.5	7.6	538	1	PVR2_HUMAN	homo sapien
1486	117.5	7.6	556	1	ILR1_HUMAN	homo sapien
1487	117.5	7.6	597	1	SIGL1_PANTR	pan troglod
1488	117.5	7.6	603	2	Q9NKF5_DROME	drosophila
1489	117.5	7.6	743	2	Q6P4H5_HUMAN	homo sapien
1490	117.5	7.6	764	1	PIGR_HUMAN	homo sapien
1491	117.5	7.6	764	2	Q8IZY7_HUMAN	homo sapien
1492	117.5	7.6	764	2	Q68DB1_HUMAN	homo sapien
1493	117.5	7.6	793	2	Q4RY64_TETNG	tetraodon n
1494	117.5	7.6	848	2	Q25198_HYDAT	hydra atten
1495	117.5	7.6	1089	2	PGFRA_HUMAN	homo sapien
1496	117.5	7.6	1198	2	Q60765_CAEBR	caenorhabdi
1497	117.5	7.6	1240	1	NFASC_MOUSE	mus musculu
1498	117.5	7.6	1251	2	Q62Q54_MOUSE	mus musculu
1499	117.5	7.6	2343	2	Q5TX11_ANOGA	anopheles g
1500	117.5	7.6	6710	2	Q61SF4_CAEBR	caenorhabdi

RESULT 1
JAM1_HUMAN
ID   JAM1_HUMAN   STANDARD;   PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE   molecule 1) (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11
DE   receptor).
GN   Name=F11R; Synonyms=JAM1, JCAM; ORFNames=UNQ264/PRO301;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=99329940; PubMed=1095639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=10753840;
RA   Sobocka M.B., Sobocki T., Banerjee P., Weiss C., Rushbrook J.I.,
RA   Norin A.J., Hartwig J., Salifu M.O., Markell M.S., Babinska A.,
RA   Ehrlich Y.H., Kornecki E.;
RT   "Cloning of the human platelet F11 receptor: a cell adhesion molecule
RT   member of the immunoglobulin superfamily involved in platelet
RT   aggregation.";
RL   Blood 95:2600-2609(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [4]

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RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Wu M.-H.,
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RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP PROTEIN SEQUENCE OF 28-103 AND 123-130, AND N-GLYCOSYLATION.
RA Naik U.P., Ehrlich Y.H., Kornecki E.;
RT "Mechanisms of platelet activation by a stimulatory antibody: cross-
RT linking of a novel platelet receptor for monoclonal antibody F11 with
RT the Fc gamma RII receptor.";
RL Biochem. J. 310:155-162(1995).
RN [8]
RP PROTEIN SEQUENCE OF 28-39.
RX PubMed=15340161; DOI=10.1110/ps.0468204;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [9]
RP PROTEIN SEQUENCE OF 28-42.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
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RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
RN [10]
RP INTERACTION WITH MPDZ.
RX PubMed=11489913; DOI=10.1083/jcb.200102047;
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RT "Junctional adhesion molecule (JAM) binds to PAR-3: a possible
RT mechanism for the recruitment of PAR-3 to tight junctions.";
RL J. Cell Biol. 154:491-497(2001).
RN [11]
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RX PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA Muller W.A.;
RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT and the inflammatory response.";
RL Trends Immunol. 24:327-334(2003).

```
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity). Interacts with the ninth PDZ domain
CC       of MPDZ.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC       Localized at tight junctions of both epithelial and endothelial
CC       cells.
CC   -!- PTM: N-Glycosylated.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC       domains.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF111713; AAD42050.1; -; mRNA.
DR   EMBL; AF207907; AAF22829.1; -; mRNA.
DR   EMBL; AF172398; AAD48877.1; -; mRNA.
DR   EMBL; AL136649; CAB66584.1; -; mRNA.
DR   EMBL; AY358896; AAQ89255.1; -; mRNA.
DR   EMBL; BC001533; AAH01533.1; -; mRNA.
DR   PIR; A59406; S56749.
DR   PDB; 1NBQ; X-ray; A/B=27-233.
DR   Ensembl; ENSG00000158769; Homo sapiens.
DR   HGNC; HGNC:14685; F11R.
DR   MIM; 605721;
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
FT   SIGNAL        1     27
FT   CHAIN        28    299       Junctional adhesion molecule A.
FT   TOPO_DOM     28    238       Extracellular (Potential).
FT   TRANSMEM    239    259       Potential.
FT   TOPO_DOM    260    299       Cytoplasmic (Potential).
FT   DOMAIN       28    125       Ig-like V-type 1.
FT   DOMAIN      135    228       Ig-like V-type 2.
FT   CARBOHYD    185    185       N-linked (GlcNAc...) (Potential).
FT   DISULFID     50    109       Potential.
FT   DISULFID    153    212       Potential.
SQ   SEQUENCE   299 AA;  32583 MW;  D95DE2FBA23D2851 CRC64;

Query Match             100.0%;  Score 1544;  DB 1;  Length 299;
Best Local Similarity   100.0%;
Matches  299;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy     61 EWKFDQGSDTTRLVCYNNKITASYEDRVTFLPFGITFKSVTREDTGTYTCMVSEEGGNSYG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EWKFDQGSDTTRLVCYNNKITASYEDRVTFLPFGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy    121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy    181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
```

.T 2

Q4 HUMAN

Q6FIB4_HUMAN PRELIMINARY;   PRT;   299 AA.

Q6FIB4;

05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

P11R protein (F11 receptor protein) (JAM1) (Hypothetical protein
FLJ90671).

Name=F11R; ORFNames=RP11-544M22.2-001;

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.

NCBI_TaxID=9606;
[1]

NUCLEOTIDE SEQUENCE.
Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
[2]

NUCLEOTIDE SEQUENCE.
MEDLINE=20537956; PubMed=11087121; DOI=10.1080/15216540050176593;
Gupta S.K., Pillarisetti K., Ohlstein E.H.;
"Platelet agonist F11 receptor is a member of the immunoglobulin
superfamily and identical with junctional adhesion molecule (JAM):
regulation of expression in human endothelial cells and macrophages.";
IUBMB Life 50:51-56(2000).
[3]

NUCLEOTIDE SEQUENCE.
MEDLINE=22701983; PubMed=12817473; DOI=10.1515/BC.2003.085;
Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W.,
Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.;
"Identification and characterization of KAT, a novel gene
preferentially expressed in several human cancer cell lines.";
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[4]

NUCLEOTIDE SEQUENCE.
TISSUE=Placenta;
Ozeuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
Nakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
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Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
capped cDNA Libraries.";
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NUCLEOTIDE SEQUENCE.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
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Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector.";
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
[6]

NUCLEOTIDE SEQUENCE.
Harrison B.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; CR533512; CAG38543.1; -; mRNA.
EMBL; AF191495; AAG28379.1; -; mRNA.
EMBL; AF490407; AAO84556.1; -; Genomic_DNA.
EMBL; BT020103; AAV38906.1; -; mRNA.
EMBL; AL591806; CAI15365.1; -; Genomic_DNA.
EMBL; AK075152; BAC11436.1; -; mRNA.
IMR; Q6FIB4; 25-233.

Ensembl; ENSG00000158769; Homo sapiens.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_c2.
InterPro; IPR003598; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00408; IGc2; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
Receptor.

SEQUENCE   299 AA;   32583 MW;   D95DE2FEA23D2851 CRC64;

Query Match   100.0%;   Score 1544;   DB 2;   Length 299;
Best Local Similarity   100.0%;   Pred. No. 1.8e-111;
Matches 299;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1   MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSBPEVRIPENNPVKLSCAYSGFSSPRV   60
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSBPEVRIPENNPVKLSCAYSGFSSPRV   60

Qy   61   EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG   120
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG   120

Qy   121   EVKVKLIVLPVPPSKPTVNIPSSATIGNRAVLTCSBQDGSPPSEYTWFKDGIVMPTNPKST   180
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121   EVKVKLIVLPVPPSKPTVNIPSSATIGNRAVLTCSBQDGSPPSEYTWFKDGIVMPTNPKST   180

Qy   181   RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCRARNGYGTPMTSNAVRMEAVERNVGVIV   240
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181   RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCRARNGYGTPMTSNAVRMEAVERNVGVIV   240

Qy   241   AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGBPFKQTSSFLV   299
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241   AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGBPFKQTSSFLV   299

RESULT 3

Q9Y5B2_HUMAN

Q9Y5B2_HUMAN PRELIMINARY;   PRT;   259 AA.

Q9Y5B2;

01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Junction adhesion molecule.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.

NCBI_TaxID=9606;
[1]

NUCLEOTIDE SEQUENCE.
Liu Y., Nurat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
Foley C., Parkos C.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

EMBL; AF154005; AAD43794.1; -; mRNA.
HSSP; Q9Y624; 1NBQ.
SMR; Q9Y5B2; 20-193.
Ensembl; ENSG00000158769; Homo sapiens.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane.

SEQUENCE   259 AA;   28122 MW;   FE38521A9115B2D0 CRC64;

Query Match   83.0%;   Score 1281;   DB 2;   Length 259;
Best Local Similarity   86.0%;   Pred. No. 3.8e-91;
Matches 257;   Conservative   0;   Mismatches   2;   Indels   40;   Gaps   2;

Qy   1   MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSBPEVRIPENNPVKLSCAYSGFSSPRV   60
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSBPEVRIPENNPVKLSCAYSGFSSPRV   60

Qy   61   EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG   120
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG   120

Qy   121   EVKVKLIVLPVPPSKPTVNIPSSATIGNRAVLTCSBQDGSPPSEYTWFKDGIVMPTNPKST   180
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121   EVKVKLIVLPVPPSKPTVNIPSSATIGNRAVLTCSBQDGSPPSEYTWFKDGIVMPTNPKST   180

Qy   181   RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCRARNGYGTPMTSNAVRMEAVERNVGVIV   240
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181   RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCRARNGYGTPMTSNAVRMEAVERNVGVIV   240

Qy   241   AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGBPFKQTSSFLV   299
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241   AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGBPFKQTSSFLV   299

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OM protein - protein search, using sw model
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
GenCore version 5.1.8

Run on: May 16, 2006, 07:02:51 ; Search time 229 Seconds
               (without alignments)
               921.192 Million cell updates/sec

Title:
Perfect score: 1544
Sequence: 1 MGTKAQVERKLLCLFILAIL.........YSQPSARSEGEFKQTSSFLV 299

Searched: US-10-785-433-1
Scoring table: 1544

Total number of hits satisfying chosen parameters: 2166443

Searched: 2166443 seqs, 705528306 residues
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 1500 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	Match DB ID	Description
1	1544	100.0	299	1	JAM1_HUMAN	Q9y624 homo sapien
2	1544	100.0	299	2	Q6FIB4_HUMAN	Q6fib4 homo sapien
3	1281	83.0	259	2	Q9Y5B2_HUMAN	Q9y5b2 homo sapien
4	1176.5	76.2	298	1	JAM1_BOVIN	Q9xts6 bos taurus
5	1176.5	76.2	298	2	Q5E9V8_BOVIN	Q5e9v8 bos taurus
6	1096.5	71.0	300	2	JAM1_RAT	Q9jhy1 rattus norv
7	1079.5	69.9	300	2	JAM1_MOUSE	Q8vc39 mus musculu
8	1073.5	69.5	300	1	JAM1_MOUSE	088792 mus musculu
9	700	45.3	173	2	Q9JKD5_RAT	Q9jkd5 rattus norv
10	602.5	39.0	289	2	Q72WT0_XENLA	Q72wt0 xenopus lae
11	580.5	37.6	296	2	Q640C0_XENLA	Q640c0 xenopus lae
12	580.5	37.6	300	2	Q7SYQ7_XENLA	Q7syq7 xenopus lae
13	571.5	37.0	292	2	Q66I72_BRARE	Q66i72 brachydanio
14	560.5	36.3	291	2	Q66JI5_XENTR	Q66ji5 xenopus tro
15	534.5	34.6	260	2	Q4S8Z8_TETNG	Q4s8z8 tetraodon n
16	431	27.9	298	1	JAM2_HUMAN	P57087 homo sapien
17	424	27.5	310	1	JAM3_HUMAN	Q9bx67 homo sapien
18	411	26.6	310	2	JAM3_MOUSE	Q9d8b7 mus musculu
19	410	26.6	298	1	JAM2_MOUSE	Q9ji59 mus musculu
20	403	26.1	310	2	JAM3_RAT	068fg2 rattus norv
21	360.5	23.3	243	2	Q5ZJD1_CHICK	Q5zjd1 gallus gall
22	338	21.9	257	2	Q4S0M3_TETNG	Q4s0m3 tetraodon n
23	293	19.0	273	2	Q4RRS6_TETNG	Q4rrs6 tetraodon n
24	280.5	18.2	319	1	GPA33_MOUSE	Q9jka5 mus musculu
25	272.5	17.6	319	1	GPA33_HUMAN	Q99795 homo sapien
26	272.5	17.6	319	2	Q5VZP6_HUMAN	Q5vzp6 homo sapien
27	257.5	16.7	344	2	Q568F7_BRARE	Q568f7 brachydanio
28	232	15.0	327	1	VSIG2_HUMAN	Q96iq7 homo sapien
29	231.5	15.0	328	1	VSIG2_MOUSE	Q9zi09 mus musculu
30	220	14.2	335	2	Q9PWR4_CHICK	Q9pwr4 gallus gall
31	219	14.2	335	2	Q9YGH1_CHICK	Q9yghl gallus gall
32	216	14.0	283	2	Q4V7Q4_XENLA	Q4v7q4 xenopus lae
33	214.5	13.9	2673	2	Q96SC3_HUMAN	Q96sc3 homo sapien
34	213.5	13.8	5635	2	Q5TYR7_HUMAN	Q5tyr7 homo sapien
35	213.5	13.8	5636	2	Q96RW7_HUMAN	Q96rw7 homo sapien
36	212	13.7	335	2	Q9YGV5_CHICK	Q9ygv5 gallus gall
37	210.5	13.6	372	1	CXAR_BRARE	Q90y50 brachydanio
38	210	13.6	332	2	Q6P359_XENTR	Q6p359 xenopus tro
39	208.5	13.5	318	2	Q91664_XENLA	Q91664 xenopus lae
40	208.5	13.5	428	2	Q5U2P2_RAT	Q5u2p2 rattus norv
41	207.5	13.4	365	1	CXAR_HUMAN	P78310 homo sapien
42	207.5	13.4	365	1	CXAR_PONPY	Q5r764 pongo pygma
43	207.5	13.4	319	2	Q5DX21_HUMAN	Q5dx21 homo sapien
44	205.5	13.3	414	2	Q5VU13_HUMAN	Q5vu13 homo sapien
45	204	13.2	431	2	Q4SMH3_TETNG	Q4smh3 tetraodon n
46	202	13.1	529	2	Q5RIP6_BRARE	Q5rip6 brachydanio
47	201.5	13.1	5533	2	Q86XK7_HUMAN	Q86xk7 homo sapien
48	201	13.0	387	2	Q8VE98_MOUSE	Q8ve98 mus musculu
49	201	13.0	412	2	Q6MZS4_HUMAN	Q6mzs4 homo sapien
50	200	13.0	319	2	Q6TU80_CANFA	Q6tu80 canis famil
51	199	12.9	347	2	Q4R7W7_MACFA	Q4r7w7 macaca fasc
52	198.5	12.9	210	2	Q5XGG4_XENTR	Q5xgg4 xenopus tro
53	198	12.8	335	2	Q58B82_XENLA	Q58b82 xenopus lae
54	197	12.8	316	2	Q7TPB4_RAT	Q7tpb4 rattus norv
55	196	12.7	319	1	CXAR_BOVIN	Q9tu79 bos taurus
56	196	12.7	365	2	Q9T079_PIG	Q9tu79 sus scrofa
57	196	12.7	373	2	Q9H6B4_HUMAN	Q9h6b4 homo sapien
58	195	12.6	430	2	Q8N4F1_HUMAN	Q8n4f1 homo sapien
59	193	12.5	373	2	Q8R373_MOUSE	Q8r373 mus musculu
60	193	12.5	2528	2	Q4S2G3_TETNG	Q4s2g3 tetraodon n
61	193	12.5	3493	2	Q4R2D0_TETNG	Q4r2d0 tetraodon n
62	192.5	12.5	3198	2	Q9U8G8_MANSE	Q9u8g8 manduca sex
63	192.5	12.5	34350	2	Q8W242_HUMAN	Q8w242 homo sapien
64	192	12.4	365	1	CXAR_MOUSE	Q9r066 mus musculu
65	191.5	12.4	332	2	Q640U3_XENTR	Q640u3 xenopus tro
66	191	12.4	323	2	Q8NDD2_HUMAN	Q8ndd2 homo sapien
67	189.5	12.3	7962	2	Q10465_HUMAN	Q10465 homo sapien
68	189	12.2	365	1	CXAR_RAT	P97792 rattus norv
69	189	12.2	373	2	Q920S5_MOUSE	Q920s5 mus musculu
70	186	12.0	372	2	Q8K1G0_RAT	Q8k1g0 rattus norv
71	185.5	12.0	858	2	O18466_HIRME	018466 hirudo medi
72	185.5	12.0	1730	2	Q7YRQ7_PIG	Q7yrq7 sus scrofa
73	185.5	12.0	3950	2	Q7YRF5_CANFA	Q7yrf5 canis famil
74	183	11.9	434	2	Q4RFG0_TETNG	Q4rfg0 tetraodon n
75	182	11.8	329	2	Q8N225_HUMAN	Q8n225 homo sapien
76	182	11.8	538	2	Q29123_PIG	Q29123 sus scrofa
77	182	11.8	1340	2	Q8NDA2_HUMAN	Q8nda2 homo sapien
78	181.5	11.8	302	2	Q4T3Z1_TETNG	Q4t3z1 tetraodon n
79	181.5	11.8	862	1	CD22_MOUSE	P35329 mus musculu
80	181.5	11.8	1154	2	Q4SR22_TETNG	Q4sr22 tetraodon n
81	181	11.7	390	2	Q95K13_XENLA	Q95k13 xenopus lae
82	181	11.7	388	1	ESAM_MACFA	macaca fasc
83	181	11.7	534	1	LRTG1_HUMAN	homo sapien
84	180.5	11.7	316	2	Q5XWD3_HUMAN	Q5xwd3 homo sapien
85	180.5	11.7	2016	2	Q60XI2_HUMAN	Q60xi2 homo sapien
86	180	11.7	2224	2	Q86BQ7_DROME	Q86bq7 drosophila
87	180	11.7	1296	2	Q9U1M1_DROME	Q9u1m1 drosophila
88	179.5	11.6	181	2	Q7Q229_ANOGA	Q7q229 anopheles g
89	179	11.6	388	2	Q91665_XENLA	Q91665 xenopus lae
90	179	11.6	534	2	Q8NC34_HUMAN	Q8nc34 homo sapien
91	179	11.6	390	2	Q8NBI8_HUMAN	Q8nbi8 homo sapien
92	179	11.6	316	2	Q5ZPR3_HUMAN	Q5zpr3 homo sapien
93	179	11.6	538	2	Q28939_PIG	Q28939 sus scrofa
94	178.5	11.6	1048	2	Q7QH02_ANOGA	Q7qh02 anopheles g
95	178.5	11.6	399	2	Q9BXR1_HUMAN	Q9bxr1 homo sapien
96	178.5	11.6	316	1	VSIG4_HUMAN	VSIG4 homo sapien
97	178.5	11.6	595	2	Q9Y279_HUMAN	Q9y279 homo sapien
98	178.5	11.6	722	2	Q6ZRS5_HUMAN	Q6zrs5 homo sapien
99	178.5	11.6	779	2	Q6ZRS5_HUMAN	Q6zrs5 homo sapien
100	178	11.6	837	2	Q4KMG2_HUMAN	Q4kmg2 homo sapien
101	178	11.6	1252	2	O97136_MANSE	097136 manduca sex
102	177.5	11.5	1496	2	O97137_MANSE	097137 manduca sex
103	177.5	11.5	1256	2	Q96DN3_HUMAN	Q96dn3 homo sapien
104	177.5	11.5	1269	2	Q92626_HUMAN	Q92626 homo sapien

No.				N	Accession	Organism
105	177.5	11.5	1273	2	O44928_CAEEL	caenorhabdi
106	176	11.4	533	2	Q8NCB6_HUMAN	homo sapien
107	176	11.4	390	2	Q96AP7_HUMAN	homo sapien
108	175.5	11.4	319	1	ESAM_HUMAN	homo sapien
109	175.5	11.4	407	2	Q7QLK4_ANOGA	anopheles g
110	175.5	11.4	10495	2	Q9D2J4_TETNG	mus musculu
111	175.5	11.4	407	2	Q4RE92_TETNG	tetraodon n
112	174.5	11.3	882	2	Q4RVZ3_TETNG	tetraodon n
113	174.5	11.3	398	2	Q7Q916_ANOGA	anopheles g
114	174	11.3	1725	2	Q8N126_HUMAN	homo sapien
115	174	11.3	398	2	Q640R3_MOUSE	mus musculu
116	174	11.3	413	2	Q9UJP1_HUMAN	homo sapien
117	173.5	11.2	2293	2	Q4T1M4_TETNG	tetraodon n
118	173.5	11.2	439	2	Q6RWT6_BOVIN	bos taurus
119	173.5	11.2	1268	2	Q619L9_CAEBR	caenorhabdi
120	173.5	11.2	432	2	Q7KVK3_DROME	drosophila
121	173.5	11.2	1429	2	Q44924_DROME	drosophila
122	173	11.2	300	2	Q9W213_DROME	drosophila
123	173	11.2	367	2	Q7PV30_ANOGA	anopheles g
124	173	11.2	416	2	Q62WL4_HUMAN	homo sapien
125	173	11.2	416	2	Q8N713_HUMAN	homo sapien
126	173	11.2	1709	1	Q6TIP8_HUMAN	homo sapien
127	172.5	11.2	418	2	SN_HUMAN	homo sapien
128	172.5	11.2	1227	2	Q9BZZ2_HUMAN	homo sapien
129	172.5	11.2	1431	2	Q501T5_BRARE	brachydanio
130	172.5	11.2	399	2	Q21038_CAEEL	caenorhabdi
131	172	11.2	602	2	Q80U60_MOUSE	mus musculu
132	172	11.1	650	2	Q8N772_HUMAN	homo sapien
133	172	11.1	2597	2	Q86YJ9_HUMAN	homo sapien
134	172	11.1	2623	2	Q8NA84_HUMAN	homo sapien
135	171.5	11.1	1693	2	Q6WRI0_HUMAN	homo sapien
136	171.5	11.1	324	2	Q6WRH9_RAT	rattus norv
137	171	11.1	343	2	Q4S6A5_TETNG	tetraodon n
138	171	11.1	1091	2	Q8R4Y0_MOUSE	mus musculu
139	171	11.1	1119	1	Q7TMH2_MOUSE	mus musculu
140	171	11.1	375	2	LRIG1_MOUSE	mus musculu
141	170.5	11.1	436	2	Q6RWT4_BOVIN	bos taurus
142	170.5	11.0	2013	2	Q6VAN8_BOVIN	bos taurus
143	170.5	11.0	453	2	Q8VHZ8_RAT	rattus norv
144	170.5	11.0	595	2	Q9ERC8_MOUSE	mus musculu
145	170.5	11.0	630	2	Q4T6S3_TETNG	tetraodon n
146	170	11.0	648	2	Q5W431_FUGRU	fugu rubrip
147	170	11.0	1117	1	Q5W436_FUGRU	fugu rubrip
148	170	11.0	1460	2	LRIG3_FUGRU	fugu rubrip
149	170	11.0	452	1	Q5H261_XENTR	xenopus tro
150	170	11.0	753	2	Q4RRT0_TETNG	tetraodon n
151	169.5	11.0	765	2	Q5J7D9_MOUSE	mus musculu
152	169.5	11.0	799	2	Q9TWA4_APLCA	aplysia cal
153	169.5	11.0	799	2	Q8C3V5_MOUSE	mus musculu
154	169.5	11.0	812	2	Q9TWA5_APLCA	aplysia cal
155	169.5	11.0	881	2	Q4RQR3_TETNG	tetraodon n
156	169.5	11.0	932	2	Q9TWA6_APLCA	aplysia cal
157	169.5	11.0	932	2	Q9BKP9_APLCA	aplysia cal
158	169.5	11.0	1450	2	Q4SCT9_TETNG	tetraodon n
159	169.5	11.0	2222	2	O97394_DROME	drosophila
160	169.5	11.0	343	2	Q8BYS4_MOUSE	mus musculu
161	169	11.0	396	2	Q99N28_MOUSE	m nectin-li
162	169	10.9	739	1	VCAM1_MOUSE	mus musculu
163	169	10.9	739	2	Q91X98_MOUSE	mus musculu
164	169	10.9	739	2	Q8K0X1_MOUSE	mus musculu
165	169	10.9	1134	2	Q71B05_BRARE	brachydanio
166	169	10.9	2828	2	Q9NR99_HUMAN	homo sapien
167	168.5	10.9	432	2	Q6DDE7_XENLA	xenopus lae
168	168.5	10.9	662	2	Q60926_MOUSE	homo sapien
169	168.5	10.9	3410	2	Q7TN00_RAT	rattus norv
170	168.5	10.9	6620	2	Q96AA2_HUMAN	homo sapien
171	168.5	10.9	372	2	Q6VAN6_BOVIN	bos taurus
172	167.5	10.9	1746	2	Q8WY19_HUMAN	homo sapien
173	167.5	10.8	2012	2	DSCAM_HUMAN	homo sapien
174	167.5	10.8	2023	2	Q59GH3_HUMAN	homo sapien
175	167.5	10.8	237	2	Q6DQX5_RABIT	oryctolagus
176	167	10.8	404	2	Q4KLY3_RAT	rattus norv
177	167	10.8				

No.				N	Accession	Organism	Accession 2	Organism 2
178	166.5	10.8	394	1	ESAM_MOUSE	mus musculu	Q925f2	mus musculu
179	166.5	10.8	622	2	Q9R069_MOUSE	mus musculu	Q9r069	mus musculu
180	166.5	10.8	650	2	Q99K86_MOUSE	mus musculu	Q99k86	mus musculu
181	166.5	10.8	1038	2	Q4T3K8_TETNG	tetraodon n	Q4t3k8	tetraodon n
182	166	10.8	377	2	Q4RZV7_TETNG	tetraodon n	Q4rzv7	tetraodon n
183	166	10.8	563	2	Q5FWR8_XENTR	xenopus tro	Q5fwr8	xenopus tro
184	166	10.8	584	2	Q9Y3Y8_HUMAN	homo sapien	Q9y3y8	homo sapien
185	166	10.8	591	2	Q9NP04_DROME	drosophila	Q9np04	drosophila
186	166	10.8	2772	2	Q9VAV4_DROME	drosophila	Q9vav4	drosophila
187	166	10.8	2894	2	Q7KRX2_DROME	drosophila	Q7krx2	drosophila
188	166	10.8	5175	2	Q8IOL3_CAEEL	caenorhabdi	Q81ol3	caenorhabdi
189	166	10.8	5198	2	O76518_CAEEL	caenorhabdi	O76518	caenorhabdi
190	166	10.8	1164	2	Q66MN5_DROVI	drosophila	Q66mn5	drosophila
191	165.5	10.7	1389	2	Q98SW3_BRARE	brachydanio	Q98sw3	brachydanio
192	165.5	10.7	1419	2	Q9NBA1_DROME	drosophila	Q9nba1	drosophila
193	165.5	10.7	2016	2	Q98918_CHICK	gallus gall	Q98918	gallus gall
194	165.5	10.7	4162	2	P40199_HUMAN	homo sapien	P40199	homo sapien
195	165	10.7	344	2	CEAM6_HUMAN	homo sapien	Ceam6	homo sapien
196	165	10.7	344	2	Q53XP7_HUMAN	homo sapien	Q53xp7	homo sapien
197	165	10.7	344	1	Q13774_HUMAN	homo sapien	Q13774	homo sapien
198	165	10.7	624	2	Q9ESS6_RAT	rattus norv	Q9ess6	rattus norv
199	165	10.7	5992	2	Q9W615_CAEEL	caenorhabdi	Q9w615	caenorhabdi
200	165	10.7	6632	1	UNC89_CAEEL	caenorhabdi	Unc89	caenorhabdi
201	165	10.7	7122	2	O01761_CAEEL	caenorhabdi	O01761	caenorhabdi
202	165	10.7	7441	2	Q5W616_CAEEL	caenorhabdi	Q5w616	caenorhabdi
203	165	10.7	8081	2	Q5W617_CAEEL	caenorhabdi	Q5w617	caenorhabdi
204	164.5	10.7	432	2	Q7Z120_CAEEL	caenorhabdi	Q7z120	caenorhabdi
205	164.5	10.7	739	1	Q6RWT5_BOVIN	bos taurus	Q6rwt5	bos taurus
206	164.5	10.7	812	2	VCAM1_CANFA	canis famil	Vcam1	canis famil
207	164.5	10.7	765	2	Q9BKQ0_APLCA	aplysia cal	Q9bkq0	aplysia cal
208	164.5	10.7	1095	2	Q9BKQ0_APLCA	aplysia cal	Q9bkq0	aplysia cal
209	164.5	10.7	1109	2	Q5BEP4_BRARE	brachydanio	Q5bep4	brachydanio
210	164.5	10.7	2016	2	Q6P5H3_MOUSE	mus musculu	Q6p5h3	mus musculu
211	164.5	10.7	2016	2	Q6P5H3_MOUSE	mus musculu	Q6p5h3	mus musculu
212	164	10.7	2019	2	Q8MKM8_DROME	drosophila	Q8mkm8	drosophila
213	164	10.7	595	2	Q8MKM7_DROME	drosophila	Q8mkm7	drosophila
214	164	10.6	605	2	Q8MKM6_DROME	drosophila	Q8mkm6	drosophila
215	164	10.6	2222	2	Q4RY92_TETNG	tetraodon n	Q4ry92	tetraodon n
216	163.5	10.6	305	2	Q6P3A4_MOUSE	mus musculu	Q6p3a4	mus musculu
217	163.5	10.6	422	2	O502A9_BRARE	brachydanio	O502a9	brachydanio
218	163.5	10.6	1020	2	Q8NHN0_HUMAN	homo sapien	Q8nhn0	homo sapien
219	163.5	10.6	1083	2	O76698_CAEEL	caenorhabdi	O76698	caenorhabdi
220	163.5	10.6	2022	2	Q7KQG5_DROME	drosophila	Q7kqg5	drosophila
221	163.5	10.6	6620	2	Q5VST9_HUMAN	homo sapien	Q5vst9	homo sapien
222	163	10.6	249	1	Q58DG9_BOVIN	bos taurus	Q58dg9	bos taurus
223	163	10.6	335	2	Q5XKA0_XENLA	xenopus lae	Q5xka0	xenopus lae
224	163	10.6	520	2	Q925P2_MOUSE	mus musculu	Q925p2	mus musculu
225	162.5	10.6	622	2	Q9ESS5_MOUSE	mus musculu	Q9ess5	mus musculu
226	162.5	10.5	622	2	Q9JKB2_MOUSE	mus musculu	Q9jkb2	mus musculu
227	162.5	10.5	779	2	Q4STG7_TETNG	tetraodon n	Q4stg7	tetraodon n
228	162.5	10.5	931	2	Q6KAM5_MOUSE	mus musculu	Q6kam5	mus musculu
229	162.5	10.5	1102	2	Q923W7_MOUSE	mus musculu	Q923w7	mus musculu
230	162.5	10.5	1102	2	Q8CE91_MOUSE	mus musculu	Q8ce91	mus musculu
231	162.5	10.5	1109	2	Q6AZB0_MOUSE	mus musculu	Q6azb0	mus musculu
232	162.5	10.5	1109	2	Q8CE73_MOUSE	mus musculu	Q8ce73	mus musculu
233	162	10.5	1110	1	ESAM_RAT	rattus norv	Esam	rattus norv
234	162	10.5	394	1	Q61V11_CAEBR	caenorhabdi	Q61v11	caenorhabdi
235	162	10.5	699	2	Q90YM0_BRARE	brachydanio	Q90ym0	brachydanio
236	162	10.5	795	2	Q4SST3_TETNG	tetraodon n	Q4sst3	tetraodon n
237	162	10.5	862	2	Q4TAD5_TETNG	tetraodon n	Q4tad5	tetraodon n
238	161.5	10.5	1090	2	Q69YJ3_HUMAN	homo sapien	Q69yj3	homo sapien
239	161.5	10.5	1244	2	Q6VAN7_BOVIN	bos taurus	Q6van7	bos taurus
240	161.5	10.5	1048	2	Q7QH01_ANOGA	anopheles g	Q7qh01	anopheles g
241	161	10.5	2174	2	Q9GQRO_DROME	drosophila	Q9gqro	drosophila
242	161	10.4	493	2	Q9P5Y4_HUMAN	homo sapien	Q9p5y4	homo sapien
243	161	10.4	650	2	Q9GKR2_BOVIN	bos taurus	Q9gkr2	bos taurus
244	161	10.4	735	2	Q4RZE9_TETNG	tetraodon n	Q4rze9	tetraodon n
245	161	10.4	739	2	Q9GKR3_BOVIN	bos taurus	Q9gkr3	bos taurus
246	160.5	10.4	190	2	Q4SA11_TETNG	tetraodon n	Q4sa11	tetraodon n
247	160.5	10.4	368	2	Q6RWT3_BOVIN	bos taurus	Q6rwt3	bos taurus
248	160.5	10.4	4071	2	Q6KDZ1_CHICK	gallus gall	Q6kdz1	gallus gall
249	160	10.4	448	2	Q8IGA5_DROME	drosophila	Q8iga5	drosophila
250	160	10.4	1051	1	PTK7_CHICK	gallus gall	Ptk7	gallus gall

No.					ID	Organism
251	160	10.4	1288	2	Q624K5_CAEBR	caenorhabdi
252	160	10.4	1328	2	Q21043_CAEEL	caenorhabdi
253	160	10.4	1614	2	Q8UVD7_XENLA	xenopus lae
254	160	10.4	2776	2	Q869A0_DROME	drosophila
255	160	10.4	2898	2	Q86829_DROME	drosophila
256	159.5	10.3	397	2	Q6XRC3_HUMAN	homo sapien
257	159.5	10.3	1032	2	Q8UVD6_BRARE	brachydanio
258	159.5	10.3	1056	2	Q90Z03_XENLA	xenopus lae
259	159.5	10.3	1140	2	Q4RRD1_TETNG	tetraodon n
260	159.5	10.3	1443	2	Q8MTB2_DROME	drosophila
261	159.5	10.3	1765	2	Q9VS30_DROME	drosophila
262	159.5	10.3	1770	2	Q9VS29_DROME	drosophila
263	159.5	10.3	2419	2	Q7PXZ1_ANOGA	anopheles g
264	159	10.3	226	2	Q4RDM1_TETNG	tetraodon n
265	159	10.3	300	2	Q9D9J0_MOUSE	mus musculu
266	159	10.3	344	2	Q99PJ0_MOUSE	mus musculu
267	159	10.3	344	1	NTRI_MOUSE	mus musculu
268	159	10.3	433	2	Q8BG33_MOUSE	mus muscu
269	159	10.3	538	2	Q9V644_DROME	drosophila
270	159	10.3	1006	2	Q9QYQ7_MOUSE	mus musculu
271	159	10.3	1827	2	Q6ID69_DROME	drosophila
272	159	10.3	2008	2	Q9VSG5_DROME	drosophila
273	159	10.3	2046	2	Q9VEJ5_DROME	drosophila
274	159	10.3	3347	2	Q7KSE9_DROME	drosophila
275	159	10.3	3354	2	Q8MMJ9_BOMMO	bombyx mori
276	158.5	10.3	330	2	Q8T101_BOMMO	bombyx mori
277	158.5	10.3	437	2	P97269_CAVPO	cavia porce
278	158.5	10.3	977	2	Q8NF56_HUMAN	homo sapien
279	158.5	10.3	977	2	Q96RD9_HUMAN	homo sapien
280	158	10.2	875	2	Q5VYK9_HUMAN	homo sapien
281	158	10.2	1040	1	Q4RRR9_TETNG	tetraodon n
282	158	10.2	1040	2	CNTN2_HUMAN	homo sapien
283	158	10.2	1040	2	Q5T054_HUMAN	homo sapien
284	158	10.2	1062	2	Q5RDT8_PONPY	pongo pygma
285	158	10.2	1091	1	Q8BKG3_MOUSE	mus musculu
286	158	10.2	1302	1	NCAM1_CHICK	gallus gall
287	158	10.2	1379	2	NRG_DROME	drosophila
288	157.5	10.2	345	2	Q58DA5_BOVIN	bos taurus
289	157.5	10.2	365	2	Q6VAN5_BOVIN	bos taurus
290	157.5	10.2	433	2	Q6DJ83_XENTR	xenopus tro
291	157.5	10.2	639	2	Q96P30_HUMAN	homo sapien
292	157.5	10.2	707	2	Q5VXZ8_HUMAN	homo sapien
293	157.5	10.2	719	2	Q66IV0_XENLA	xenopus lae
294	157.5	10.2	725	2	O73633_XENLA	xenopus lae
295	157.5	10.2	727	1	Q6RKB2_RAT	rattus norv
296	157.5	10.2	734	2	Q96LA4_HUMAN	homo sapien
297	157.5	10.2	734	2	Q96P31_HUMAN	homo sapien
298	157.5	10.2	742	1	Q8N6S2_HUMAN	homo sapien
299	157.5	10.2	837	1	NCAM2_HUMAN	homo sapien
300	157	10.2	837	2	Q6RKB3_RAT	rattus norv
301	157	10.2	837	2	NCA11_HUMAN	homo sapien
302	157	10.2	1088	1	Q4RRT1_TETNG	tetraodon n
303	157	10.2	1098	2	O08476_CHICK	gallus gall
304	157	10.2	1323	2	Q4SQ01_TETNG	tetraodon n
305	157	10.2	235	2	NCAM2_MOUSE	mus musculu
306	157	10.2	337	2	P97268_CAVPO	cavia porce
307	157	10.2	344	2	NTRI_HUMAN	homo sapien
308	157	10.2	406	2	Q8N7T8_HUMAN	homo sapien
309	157	10.2	846	2	Q9P121_HUMAN	homo sapien
310	157	10.2	1100	2	Q21041_CAEEL	caenorhabdi
311	157	10.2	1199	2	Q57576_CYNPY	cynops pyrr
312	157	10.2	2169	2	Q57577_CYNPY	cynops pyrr
313	156.5	10.1	208	2	Q8AV58_CHICK	gallus gall
314	156.5	10.1	300	2	Q80WN3_MOUSE	mus musculu
315	156.5	10.1	345	2	Q68SP0_MOUSE	mus musculu
316	156.5	10.1	778	2	Q81IH7_MOUSE	mus musculu
317	156.5	10.1	778	1	KIRR3_MOUSE	mus musculu
318	156.5	10.1	829	1	KIRR3_HUMAN	homo sapien
319	156.5	10.1	1348	1	Q4RIG0_TETNG	tetraodon n
320	156.5	10.1	1386	1	Q67M1_CHICK	gallus gall
321	156	10.1	2213	2	ROBO3_HUMAN	homo sapien
322	156	10.1	300	2	Q7Z5N4_HUMAN	homo sapien
323	156	10.1	368	2	Q9DA22_MOUSE	mus musculu

No.					ID	Organism	Accession
324	156	10.1	387	1	SIG13_PANTR	pan troglod	Q6j4a4
325	156	10.1	865	2	Q68DA2_HUMAN	homo sapien	Q68da2
326	156	10.1	931	2	Q8NF26_HUMAN	homo sapien	Q8nf26
327	156	10.1	997	2	Q44087_CAEEL	caenorhabdi	Q44087
328	156	10.1	1028	1	CNTN6_MOUSE	mus musculu	Q9jmb8
329	156	10.1	1040	2	Q22063_RAT	rattus norv	Q22063
330	156	10.1	1259	2	Q9CGJ3_MOUSE	mus musculu	Q9cgj3
331	156	10.1	1264	2	P91767_MANSE	manduca sex	P91767
332	156	10.1	2295	2	Q61GU4_CAEBR	caenorhabdi	Q61gu4
333	156	10.1	521	2	Q61352_MOUSE	mus musculu	Q61352
334	155.5	10.1	525	2	Q5R9N6_PONPY	pongo pygma	Q5r9n6
335	155.5	10.1	803	2	Q802F5_RAT	rattus norv	Q802f5
336	155.5	10.1	808	1	FGFR4_MOUSE	mus musculu	Q03142
337	155.5	10.1	811	2	Q9YH43_XENLA	xenopus lae	Q9yh43
338	155.5	10.1	837	2	Q7Z7F2_HUMAN	homo sapien	Q7z7f2
339	155.5	10.1	858	2	P13596_CHICK	gallus gall	P13596
340	155.5	10.1	1499	2	NCAM1_RAT	rattus norv	P13595
341	155	10.1	265	2	Q90815_CHICK	gallus gall	Q90815
342	155	10.0	344	1	Q9NGZ0_SPOFR	spodoptera	Q9ngz0
343	155	10.0	601	2	Q5R554_PONPY	pongo pygma	Q5r554
344	155	10.0	641	2	Q9C6J3_HUMAN	homo sapien	Q9c6j3
345	155	10.0	816	2	Q86SD2_CIOIN	ciona inte	Q86sd2
346	155	10.0	858	2	Q8NFA5_HUMAN	homo sapien	Q8nfa5
347	155	10.0	943	2	Q86X47_HUMAN	homo sapien	Q86x47
348	155	10.0	1070	2	Q7PRK4_ANOGA	anopheles g	Q7prk4
349	155	10.0	1070	2	Q6IG54_HUMAN	homo sapien	Q6ig54
350	155	10.0	1089	2	Q5T650_HUMAN	homo sapien	Q5t650
351	155	10.0	1280	2	Q4SS56_TETNG	tetraodon n	Q4ss56
352	155	10.0	1748	2	Q4RRJ3_TETNG	tetraodon n	Q4rrj3
353	154.5	10.0	442	2	Q43GQ6_TETNG	tetraodon n	Q43gq6
354	154.5	10.0	521	2	Q6NW88_BRARE	brachydanio	Q6nw88
355	154.5	10.0	527	2	Q925P3_MOUSE	mus musculu	Q925p3
356	154.5	10.0	605	2	Q4SZU1_TETNG	tetraodon n	Q4szu1
357	154.5	10.0	725	2	Q92IP2_MOUSE	mus musculu	Q92ip2
358	154.5	10.0	838	2	Q5I2D5_CANFA	canis famil	Q5i2d5
359	154.5	10.0	690	1	Q8BQ96_MOUSE	mus musculu	Q8bq96
360	154.5	10.0	847	2	Q8C4B2_MOUSE	mus musculu	Q8c4b2
361	154.5	10.0	1675	2	VCAM1_RAT	rattus norv	P29534
362	154.5	10.0	1759	2	Q5FVS3_RAT	rattus norv	Q5fvs3
363	154.5	10.0	2053	1	NCA12_HUMAN	homo sapien	P13592
364	154.5	10.0	1516	2	Q7PPH8_ANOGA	anopheles g	Q7pph8
365	154	10.0	461	2	Q8TD84_HUMAN	homo sapien	Q8td84
366	154	10.0	633	2	DSCL1_HUMAN	homo sapien	Q59fl7
367	154	10.0	651	2	Q72Z48_BRARE	brachydanio	Q72z48
368	154	10.0	690	2	Q13854_HUMAN	homo sapien	Q13854
369	154	10.0	739	1	Q5W434_BRARE	brachydanio	Q5w434
370	154	10.0	739	2	Q5W433_BRARE	brachydanio	Q5w433
371	154	10.0	761	2	Q5I8L0_MACFA	macaca fasc	Q5i8l0
372	154	10.0	807	2	Q51D07_CANFA	canis famil	Q51d07
373	154	10.0	848	2	Q59F17_HUMAN	homo sapien	Q59f17
374	154	10.0	1070	1	PTK7_HUMAN	homo sapien	PTK7
375	154	10.0	1248	2	Q9XT41_CERAE	cercopithec	Q9xt41
376	154	10.0	1256	2	O35158_RAT	rattus norv	O35158
377	153.5	9.9	394	2	Q9ZXX1_XENLA	xenopus lae	Q9zxx1
378	153.5	9.9	550	2	Q72ZX1_XENLA	xenopus lae	Q72zx1
379	153.5	9.9	582	2	Q9VMN9_DROME	drosophila	Q9vmn9
380	153.5	9.9	739	2	Q8R4B5_MOUSE	oryctolagus	Q8r4b5
381	153.5	9.9	853	1	Q865F2_RABIT	bos taurus	Q865f2
382	153.5	9.9	915	2	NCAM1_BOVIN	bos taurus	P31836
383	153.5	9.9	1043	2	Q8R4B3_MOUSE	mus musculu	Q8r4b3
384	153.5	9.9	1060	2	Q9Q2I3_RAT	rattus norv	Q9q2i3
385	153.5	9.9	1209	2	Q7PG72_ANOGA	anopheles g	Q7pg72
386	153.5	9.9	1215	2	Q7OEC1_ANOGA	anopheles g	Q7oec1
387	153.5	9.9	2024	1	Q53CM6_BRARE	brachydanio	Q53cm6
388	153	9.9	344	1	NTRI_RAT	rattus norv	Q62718
389	153	9.9	545	2	Q7QIV4_ANOGA	anopheles g	Q7qiv4
390	153	9.9	588	2	Q4RFF0_TETNG	tetraodon n	Q4rff0
391	153	9.9	590	2	Q7O1V4_TETNG	tetraodon n	Q7o1v4
392	153	9.9	912	1	Q4SZG4_TETNG	tetraodon n	Q4szg4
393	153	9.9	1005	2	Q4SPP8_TETNG	tetraodon n	Q4spp8
394	153	9.9	1028	2	CNTN6_RAT	rattus norv	P97528
395	153	9.9	1260	2	P79921_XENLA	xenopus lae	P79921
396	153	9.9	1338	1	VGFR1_HUMAN	h vascular	P17948

#	Score		Len	N	Name	Accession	Organism
397	153	9.9	1338	2	Q5tar1_HUMAN	q5tar1	homo sapien
398	152.5	9.9	342	2	Q642g9_BRARE	q642g9	brachydanio
399	152.5	9.9	554	2	Q9w4r3_DROME	q9w4r3	drosophila
400	152.5	9.9	821	2	Q9yh44_XENLA	q9yh44	xenopus lae
401	152.5	9.9	843	2	Q5ea96_BOVIN	q5ea96	bos taurus
402	152.5	9.9	857	2	Q5i2d6_CANFA	q5i2d6	canis famil
403	152.5	9.9	920	2	Q4rsg7_TETNG	q4rsg7	tetraodon n
404	152.5	9.9	1225	2	Q6gp61_XENLA	q6gp61	xenopus lae
405	152.5	9.9	1332	2	Q9bn17_DROME	q9bn17	drosophila
406	152.5	9.9	1332	2	Q9vqw7_DROME	q9vqw7	drosophila
407	152	9.8	338	1	LSAMP_HUMAN	q13449	homo sapien
408	152	9.8	534	2	Q86se4_HUMAN	q86se4	homo sapien
409	152	9.8	534	2	Q86t2_PANTR	q86t2	pan troglod
410	152	9.8	838	2	Q4spp9_TETNG	q4spp9	tetraodon n
411	152	9.8	891	2	Q25177_HYDAT	q25177	hydra atten
412	152	9.8	1036	1	CNTN2_CHICK	p28685	gallus gall
413	152	9.8	1114	2	Q9bwv1_HUMAN	q9bwv1	homo sapien
414	152	9.8	1115	2	Q6uxj5_HUMAN	q6uxj5	homo sapien
415	152	9.8	1255	2	Q7z329_HUMAN	q7z329	homo sapien
416	152	9.8	1257	1	Q7yql8_PANTR	q7yql8	pan troglod
417	152	9.8	1257	1	L1CAM_HUMAN	p32004	homo sapien
418	152	9.8	1443	1	NEO1_CHICK	q90610	gallus gall
419	151.5	9.8	458	2	Q61351_MOUSE	q61351	mus musculu
420	151.5	9.8	581	2	Q4syi7_TETNG	q4syi7	tetraodon n
421	151.5	9.8	725	1	NCA12_MOUSE	p13594	mus musculu
422	151.5	9.8	740	1	Q96p29_HUMAN	q96p29	homo sapien
423	151.5	9.8	838	2	Q90ym1_BRARE	q90ym1	brachydanio
424	151.5	9.8	846	2	Q5r1q0_FELCA	q5r1q0	felis silve
425	151.5	9.8	847	1	Q5g7g8_FELCA	q5g7g8	felis silve
426	151.5	9.8	1028	2	CNTN6_HUMAN	q9ug52	homo sapien
427	151.5	9.8	1028	1	Q6inb5_XENLA	q6inb5	xenopus lae
428	151.5	9.8	1033	2	Q9v643_DROME	q9v643	drosophila
429	151.5	9.8	1115	2	NCA11_MOUSE	p13595	mus musculu
430	151.5	9.8	3707	2	PGBM_MOUSE	q05793	mus musculu
431	151	9.8	442	2	Q6kat6_MOUSE	q6kat6	mus musculu
432	151	9.8	749	2	Q967d9_DROME	q967d9	drosophila
433	151	9.8	902	2	Q8iq17_DROME	q8iq17	drosophila
434	151	9.8	903	2	Q9vqy1_DROME	q9vqy1	drosophila
435	151	9.8	903	2	Q967d8_DROME	q967d8	drosophila
436	151	9.8	1249	2	Q90z04_XENLA	q90z04	xenopus lae
437	151	9.8	1508	2	Q6nr34_DROME	q6nr34	drosophila
438	151	9.8	1508	2	Q9vgy2_DROME	q9vgy2	drosophila
439	151	9.8	1531	2	Q967d7_DROME	q967d7	drosophila
440	150.5	9.8	265	1	CEAM7_HUMAN	o14002	homo sapien
441	150.5	9.7	349	1	CEAM8_HUMAN	p31997	homo sapien
442	150.5	9.7	395	2	Q8bzp4_MOUSE	q8bzp4	mus musculu
443	150.5	9.7	395	2	Q8bxj7_MOUSE	q8bxj7	m mus muscu
444	150.5	9.7	404	2	Q8blq9_MOUSE	q8blq9	mus musculu
445	150.5	9.7	521	1	CEAM1_MOUSE	p31809	mus musculu
446	150.5	9.7	1028	2	Q5r6d4_PONPY	q5r6d4	pongo pygma
447	150.5	9.7	1033	2	Q24327_DROME	q24327	drosophila
448	150.5	9.7	1501	2	Q9qw00_9MURI	q9qw00	rattus sp.
449	150.5	9.7	1501	2	Q4jfl8_RAT	q4jfl8	rattus norv
450	150.5	9.7	1561	2	Q924d2_MOUSE	q924d2	mus musculu
451	150.5	9.7	1788	2	Q9iaj0_XENLA	q9iaj0	xenopus lae
452	150.5	9.7	1863	2	Q64605_RAT	q64605	rattus norv
453	150.5	9.7	3165	2	Q7q767_ANOGA	q7q767	anopheles g
454	150	9.7	376	2	Q90zr1_BRARE	q90zr1	brachydanio
455	150	9.7	508	1	PCRL2_HUMAN	q961a5	homo sapien
456	150	9.7	702	1	CEAM5_HUMAN	p06731	homo sapien
457	150	9.7	702	2	Q8n4d0_HUMAN	q8n4d0	homo sapien
458	150	9.7	1040	1	CNTN2_HUMAN	q61330	homo sapien
459	150	9.7	2693	2	Q8isf3_CAEEL	q8isf3	caenorhabdi
460	150	9.7	2708	2	Q8isf4_CAEEL	q8isf4	caenorhabdi
461	150	9.7	16215	2	Q9nfs3_DROME	q9nfs3	drosophila
462	150	9.7	18074	2	Q9i7u4_DROME	q9i7u4	drosophila
463	150	9.7	18519	2	Q8isf6_CAEEL	q8isf6	caenorhabdi
464	150	9.7	18534	2	Q8isf7_CAEEL	q8isf7	caenorhabdi
465	149.5	9.7	234	2	Q78t27_MOUSE	q78t27	mus musculu
466	149.5	9.7	291	2	Q6580q7_HUMAN	q6580q7	homo sapien
467	149.5	9.7	337	1	OBCAM_CHICK	o8cam	gallus gall
468	149.5	9.7	344	2	Q9df61_CHICK	q9df61	gallus gall
469	149.5	9.7	725	2	O73634_XENLA	o73634	xenopus lae
470	149.5	9.7	1030	2	Q8nfa8_HUMAN	q8nfa8	homo sapien
471	149.5	9.7	1497	2	Q5xjv4_MOUSE	q5xjv4	mus musculu
472	149.5	9.7	1501	2	Q7tt17_MOUSE	q7tt17	mus musculu
473	149.5	9.7	1904	2	Q64699_MOUSE	q64699	mus musculu
474	149.5	9.7	1907	2	Q4jfc7_MOUSE	q4jfc7	mus musculu
475	149.5	9.7	359	1	LACH_DROME	q24372	drosophila
476	149	9.7	437	2	Q7qg58_ANOGA	q7qg58	anopheles g
477	149	9.7	450	2	Q6ux10_HUMAN	q6ux10	homo sapien
478	149	9.7	476	1	Q7zxj8_XENLA	q7zxj8	xenopus lae
479	149	9.7	526	1	CEAM1_HUMAN	p13688	homo sapien
480	149	9.7	739	1	VCAM1_HUMAN	p19320	homo sapien
481	149	9.7	739	1	Q90ym2_BRARE	q90ym2	brachydanio
482	149	9.7	1031	2	Q7yql7_PONPY	q7yql7	pongo pygma
483	149	9.7	1255	2	Q7qgt8_ANOGA	q7qgt8	anopheles g
484	149	9.7	1937	2	Q13332_HUMAN	q13332	homo sapien
485	149	9.7	1948	1	PTPRS_HUMAN	p98160	homo sapien
486	149	9.7	4391	1	PGBM_HUMAN	p98160	homo sapien
487	149	9.7	591	2	Q5vu27_HUMAN	q5vu27	homo sapien
488	148.5	9.7	650	2	Q4t2m0_TETNG	q4t2m0	tetraodon n
489	148.5	9.7	650	2	Q63709_9MURI	q63709	rattus sp.
490	148.5	9.6	885	2	Q8hyv1_PIG	q8hyv1	sus scrofa
491	148.5	9.6	886	2	Q8hyv2_PIG	q8hyv2	sus scrofa
492	148.5	9.6	955	2	MDGA1_HUMAN	q8nfp4	homo sapien
493	148.5	9.6	972	2	Q26614_STRPU	q26614	strongyloce
494	148.5	9.6	1378	1	Q9hck4_HUMAN	q9hck4	homo sapien
495	148.5	9.6	1534	2	ROBO2_HUMAN	o13332	homo sapien
496	148.5	9.6	2224	2	Q4rrj4_TETNG	q4rrj4	tetraodon n
497	148	9.6	231	2	Q4sln7_TETNG	q4sln7	tetraodon n
498	148	9.6	287	2	Q4sin7_TETNG	q4sin7	tetraodon n
499	148	9.6	302	2	Q7pni4_ANOGA	q7pni4	anopheles g
500	148	9.6	606	2	Q4t4k0_TETNG	q4t4k0	tetraodon n
501	148	9.6	650	2	Q4t054_TETNG	q4t054	tetraodon n
502	148	9.6	1021	2	Q4sl89_TETNG	q4sl89	tetraodon n
503	148	9.6	1100	1	CNTN5_HUMAN	o94779	homo sapien
504	148	9.6	1406	2	Q6zni1_HUMAN	q6zni1	homo sapien
505	148	9.6	1463	2	Q9gpp7_DROME	q9gpp7	drosophila
506	148	9.6	1612	2	Q9vq08_DROME	q9vq08	drosophila
507	147.5	9.6	946	1	O07153_TORCA	o07153	torpedo cal
508	147.5	9.6	509	2	ROBO1_MOUSE	o89026	mus musculu
509	147.5	9.6	677	2	O89026_MOUSE	o89026	mus musculu
510	147.5	9.5	473	1	LRIG2_HUMAN	q94898	homo sapien
511	147.5	9.6	413	1	NCA12_XENLA	p36335	xenopus lae
512	147	9.5	400	2	P36335_DROME	p36335	drosophila
513	147	9.5	353	2	P15364_DROME	p15364	drosophila
514	147	9.5	341	2	AMAL_DROME	p15364	drosophila
515	147	9.5	333	2	Q7ksx2_DROME	q7ksx2	drosophila
516	147	9.5	1092	1	CEPU1_CHICK	o90773	gallus gall
517	147	9.5	1065	2	Q90773_CHICK	q90773	gallus gall
518	147	9.5	1210	2	Q4t054_TETNG	q4t054	tetraodon n
519	147	9.5	1224	2	Q7pqf4_ANOGA	q7pqf4	anopheles g
520	147	9.5	1367	2	Q4shh6_TETNG	q4shh6	tetraodon n
521	147	9.5	1515	2	Q9eqi7_MOUSE	q9eqi7	mus musculu
522	147	9.5	1898	2	Q6v3a4_MOUSE	q6v3a4	mus musculu
523	147	9.5	1933	2	Q6pal2_MOUSE	q6pal2	mus musculu
524	146.5	9.5	2159	2	Q5tqn9_ANOGA	q5tqn9	anopheles g
525	146.5	9.5	317	2	Q61354_MOUSE	q61354	mus musculu
526	146.5	9.5	341	2	Q8byp1_MOUSE	q8byp1	mus musculu
527	146.5	9.5	404	2	Q91w54_MOUSE	q91w54	mus musculu
528	146.5	9.5	454	1	L1CAM_RAT	q05695	rattus norv
529	146.5	9.5	1287	2	Q4kmg0_HUMAN	q4kmg0	homo sapien
530	146.5	9.5	1651	1	SN_MOUSE	q62230	mus musculu
531	146.5	9.5	1694	2	Q7rtl4_DROME	q7rtl4	drosophila
532	146	9.5	17903	2	Q53g30_HUMAN	q53g30	homo sapien
533	146	9.5	702	2	FGFR4_HUMAN	p22455	homo sapien
534	146	9.5	702	2	Q8tda0_HUMAN	q8tda0	homo sapien
535	146	9.5	802	2	Q9vme2_DROME	q9vme2	drosophila
536	146	9.5	802	2	Q9vme2_DROME	q9vme2	drosophila
537	146	9.5	948	1	L1CAM_RAT	q05695	rattus norv
538	146	9.5	1259	2	Q05695_CAEEL	q05695	caenorhabdi
539	146	9.5	1479	2	Q9v4y0_DROME	q9v4y0	drosophila
540	146	9.5	1482	2	Q9kqt5_DROME	q9kqt5	drosophila
541	145.5	9.4	1914	2	Q5my99_HUMAN	q5my99	homo sapien
542	145.5	9.4	313	2	Q6vzr6_CNPV	q6vzr6	canarypox v
543	145.5	9.4	375	2	Q4s919_TETNG	q4s919	tetraodon n
544	145.5	9.4	443	2	Q9w7a9_BRARE	q9w7a9	brachydanio

Sequence listing (continued)

Entries 543–615

No.	Score	E	Entry	Accession	Organism
543	145.5	9.4	Q25403_LYMST	Q25403	lymnaea sta
544	145.5	9.4	LRIG2_MOUSE	Q52kr2	mus musculu
545	145.5	9.4	Q4S2F2_TETNG	Q4s2f2	tetraodon n
546	145.5	9.4	ROBO2_MOUSE	Q7tpd3	mus musculu
547	145.5	9.4	57596_CHICK	57596	gallus gall
548	145	9.4	Q9DGI5_CHICK	Q9dgi5	gallus gall
549	145	9.4	Q93242_CHICK	Q93242	gallus gall
550	145	9.4	Q4VWU5_XENLA	Q4vwu5	xenopus lae
551	145	9.4	Q5RJH4_MOUSE	Q5rjh4	mus musculu
552	145	9.4	NEO1_RAT	P97603	rattus norv
553	145	9.4	PTPRD_HUMAN	P23468	homo sapien
554	145	9.4	Q7Z4J0_HUMAN	Q7z4j0	homo sapien
555	144.5	9.4	Q5TNU9_ANOGA	Q5tnu9	anopheles g
556	144.5	9.4	LACH_SCHAM	Q26474	schistocerc
557	144.5	9.4	Q4V5E0_DROME	Q4v5e0	drosophila
558	144.5	9.4	Q9VMN6_DROME	Q9vmn6	drosophila
559	144.5	9.4	Q53HD1_HUMAN	Q53hd1	homo sapien
560	144.5	9.4	Q8NHN8_HUMAN	Q8nhn8	homo sapien
561	144.5	9.4	VGFR1_RAT	P53767	rattus norv
562	144.5	9.4	Q5W9G3_HUMAN	Q5w9g3	homo sapien
563	144.5	9.4	PTPRF_HUMAN	P10586	homo sapien
564	144.5	9.4	Q86WS0_HUMAN	Q86ws0	homo sapien
565	144.5	9.4	Q5T021_HUMAN	Q5t021	homo sapien
566	144.5	9.4	Q5SPJ6_MOUSE	Q5spj6	mus musculu
567	144.5	9.4	Q5T022_HUMAN	Q5t022	homo sapien
568	144.5	9.4	Q5W9G2_HUMAN	Q5w9g2	homo sapien
569	144	9.3	CEAM1_RAT	P16573	rattus norv
570	144	9.3	Q70864_ANOGA	Q70864	anopheles g
571	144	9.3	Q8WP58_DROSI	Q8wp58	drosophila
572	144	9.3	Q8WP94_DROSI	Q8wp94	drosophila
573	144	9.3	Q6PG47_HUMAN	Q6pg47	homo sapien
574	144	9.3	Q86XY3_HUMAN	Q86xy3	homo sapien
575	144	9.3	ROBO3_MOUSE	Q9z2i4	mus musculu
576	144	9.3	Q63ZG4_XENLA	Q63zg4	xenopus lae
577	144	9.3	Q64604_RAT	Q64604	rattus norv
578	144	9.3	Q8MLD5_DROME	Q8mld5	drosophila
579	144	9.3	MUSK_MOUSE	Q61006	mus musculu
580	144	9.3	CNTN5_MOUSE	P68500	mus musculu
581	144	9.3	Q7TMZ9_RAT	Q7tmz9	rattus norv
582	144	9.3	Q4RSG5_TETNG	Q4rsg5	tetraodon n
583	144	9.3	ROBO3_DROME	Q5u176	drosophila
584	144	9.3	Q9Z2I4_DROME	Q9z2i4	drosophila
585	144	9.3	Q86XY3_HUMAN	Q86xy3	homo sapien
586	144	9.3	Q64604_RAT	Q64604	rattus norv
587	144	9.3	Q8MLD8_DROME	Q8mld8	drosophila
588	144	9.3	Q8MLD5_DROME	Q8mld5	drosophila
589	144	9.3	Q9V7G8_DROME	Q9v7g8	drosophila
590	144	9.3	Q8MLD9_DROME	Q8mld9	drosophila
591	143.5	9.3	Q86GT1_PONPY	Q86gt1	pongo pygma
592	143.5	9.3	Q6GLZ7_XENLA	Q6glz7	xenopus lae
593	143.5	9.3	Q8N3J6_HUMAN	Q8n3j6	homo sapien
594	143.5	9.3	Q8IZP8_HUMAN	Q8izp8	homo sapien
595	143.5	9.3	SIG1L_MOUSE	Q1y57	mus musculu
596	143.5	9.3	PGRL1_HUMAN	Q8n441	homo sapien
597	143.5	9.3	Q5MY54_BRARE	Q5my54	brachydanio
598	143.5	9.3	Q8JG38_BRARE	Q8jg38	brachydanio
599	143.5	9.3	Q5MYA0_HUMAN	Q5mya0	homo sapien
600	143.5	9.3	Q9QW67_9MURI	Q9qw67	mus musculu
601	143.5	9.3	O03679_MOUSE	003679	mus musculu
602	143	9.3	Q56UH5_PETMA	Q56uh5	petromyzon
603	143	9.3	Q13984_HUMAN	Q13984	homo sapien
604	143	9.3	Q8HW98_MOUSE	Q8hw98	mus musculu
605	143	9.3	LSAMP_RAT	62813	rattus norv
606	143	9.3	Q6PJ82_HUMAN	Q6pj82	homo sapien
607	143	9.3	Q5TNT9_ANOGA	Q5tnt9	anopheles g
608	143	9.3	SHPS1_MOUSE	P97797	mus musculu
609	143	9.3	Q5VR25_DROME	Q5vr25	drosophila
610	143	9.3	Q4SEN2_TETNG	Q4sen2	tetraodon n
611	143	9.3	Q4RHT1_TETNG	Q4rht1	tetraodon n
612	143	9.3	Q9NEG0_DROME	Q9neg0	drosophila
613	143	9.3	CNTN1_CHICK	P14781	gallus gall
614	143	9.3	L1CAM_FUGRU	098902	fugu rubrip
615	143	9.3	Q9UM81_HUMAN	Q9um81	homo sapien

Entries 616–688

No.	Score	E	Entry	Accession	Organism
616	143	9.3	Q90Z70_BRARE	Q90z70	brachydanio
617	143	9.3	Q59PX6_HUMAN	Q59px6	homo sapien
618	143	9.3	MYLK_HUMAN	Q15746	homo sapien
619	143	9.3	Q68J72_APIME	Q68j72	apis mellif
620	143	9.3	Q59EG0_HUMAN	Q59eg0	homo sapien
621	143	9.3	Q42G20_HUMAN	Q42g20	homo sapien
622	143	9.3	Q8WZ53_HUMAN	Q8wz53	homo sapien
623	143	9.3	Q40IZ6_HUMAN	Q40iz6	homo sapien
624	143	9.3	Q8WZB3_HUMAN	Q8wzb3	homo sapien
625	142.5	9.2	Q99232_MOUSE	Q99232	mus musculu
626	142.5	9.2	BASI_CHICK	P17790	gallus gall
627	142.5	9.2	Q7PSJ8_ANOGA	Q7psj8	anopheles g
628	142.5	9.2	Q8BSM2_MOUSE	Q8bsm2	mus musculu
629	142.5	9.2	Q8AYP3_BRARE	Q8ayp3	brachydanio
630	142.5	9.2	Q5TF88_HUMAN	Q5tf88	homo sapien
631	142.5	9.2	Q59F30_HUMAN	Q59f30	homo sapien
632	142.5	9.2	Q4JFL6_RAT	Q4jfl6	rattus norv
633	142.5	9.2	Q4JF16_HUMAN	Q4jf16	homo sapien
634	142.5	9.2	Q5XNV9_PETMA	Q5xnv9	petromyzon
635	142.5	9.2	Q5XNV8_PETMA	Q5xnv8	petromyzon
636	142.5	9.2	Q6PDN3_MOUSE	Q6pdn3	mus musculu
637	142	9.2	Q4JFL7_RAT	Q4jfl7	rattus norv
638	142	9.2	Q6DN72_HUMAN	Q6dn72	homo sapien
639	142	9.2	Q16170_HUMAN	Q16170	homo sapien
640	142	9.2	Q92151_MOUSE	Q92151	mus musculu
641	142	9.2	Q92151_MOUSE	Q92151	mus musculu
642	142	9.2	Q7KYP5_HUMAN	Q7kyp5	homo sapien
643	142	9.2	Q96CA7_HUMAN	Q96ca7	homo sapien
644	142	9.2	Q96CA7_HUMAN	Q96ca7	homo sapien
645	142	9.2	Q9EQY5_MOUSE	Q9eqy5	mus musculu
646	142	9.2	Q51FI2_BRARE	Q51fi2	brachydanio
647	142	9.2	Q8T3E5_CABEL	Q8t3e5	caenorhabdi
648	142	9.2	Q19128_CABEL	Q19128	caenorhabdi
649	142	9.2	Q8MQ86_CABEL	Q8mq86	caenorhabdi
650	142	9.2	Q90W79_CHICK	Q90w79	gallus gall
651	142	9.2	Q61PF2_CAEBR	Q61pf2	caenorhabdi
652	142	9.2	Q597F7_BRARE	Q597f7	brachydanio
653	142	9.2	Q5TYT1_BRARE	Q5tyt1	brachydanio
654	142	9.2	Q5TYT0_BRARE	Q5tyt0	brachydanio
655	141.5	9.2	Q5D095_MOUSE	Q5d095	mus musculu
656	142	9.2	Q70KD0_ANOGA	Q70kd0	anopheles g
657	141.5	9.2	LSAMP_CHICK	Q98919	gallus gall
658	141.5	9.2	LSAMP_MOUSE	Q8blk3	mus musculu
659	141.5	9.2	Q8BLK3_MOUSE	Q8blk3	mus musculu
660	141.5	9.2	Q7QJG1_ANOGA	Q7qjg1	anopheles g
661	141.5	9.2	Q6PJS0_MOUSE	Q6pj50	mus musculu
662	141.5	9.2	Q5M960_RAT	Q5m960	rattus norv
663	141.5	9.2	Q6PJS0_MOUSE	Q6pj50	mus musculu
664	141.5	9.2	MAG_HUMAN	P20916	homo sapien
665	141.5	9.2	Q53ES7_HUMAN	Q53es7	homo sapien
666	141.5	9.2	Q5R4C0_PONPY	Q5r4c0	pongo pygma
667	141.5	9.2	Q59GD9_HUMAN	Q59gd9	homo sapien
668	141.5	9.2	CNTN4_RAT	Q2845	rattus norv
669	141.5	9.2	Q8MSR5_DROME	Q8msr5	drosophila
670	141.5	9.2	Q7TQG5_MOUSE	Q7tqg5	mus musculu
671	141.5	9.2	P97798_MOUSE	P97798	mus musculu
672	141.5	9.2	NEO1_MOUSE	055005	mus musculu
673	141.5	9.2	ROBO1_RAT	Q64487	rattus norv
674	141.5	9.2	PTPRD_MOUSE	P20916	mus musculu
675	141.5	9.2	Q80YN8_MOUSE	Q80yn8	mus musculu
676	141.5	9.2	Q81RV9_DROME	Q81rv9	drosophila
677	141.5	9.2	Q81RV7_DROME	Q81rv7	drosophila
678	141.5	9.2	Q8MPN3_DROME	Q8mpn3	drosophila
679	141.5	9.2	Q81RV8_DROME	Q81rv8	drosophila
680	141	9.1	Q5HZR6_XENLA	Q5hzr6	xenopus lae
681	141	9.1	Q4SUX1_TETNG	Q4sux1	tetraodon n
682	141	9.1	002869_CHICK	002869	gallus gall
683	141	9.1	Q62MD4_HUMAN	Q62md4	homo sapien
684	141	9.1	Q50317_BRARE	Q50317	brachydanio
685	141	9.1	Q5R847_PONPY	Q5r847	pongo pygma
686	141	9.1	Q59FV9_HUMAN	Q59fv9	homo sapien
687	141	9.1	MUSK_RAT	062838	rattus norv
688	141	9.1	Q4SBD4_TETNG	Q4sbd4	tetraodon n

No			Len	F	Accession		Organism
689	141	9.1	1319	2	Q4T8B2_TETNG	q4t8b2	tetraodon n
690	141	9.1	1461	1	NEO1_HUMAN		homo sapien
691	141	9.1	2174	1	Q7QEG7_ANOGA	q7qeg7	anopheles g
692	140.5	9.1	390	2	Q66KX2_XENLA	q66kx2	xenopus lae
693	140.5	9.1	394	2	Q8HXR7_MACMU	q8hxr7	macaca mula
694	140.5	9.1	394	2	Q8HXR9_MACFA	q8hxr9	macaca fasc
695	140.5	9.1	428	2	Q9PJ6_HUMAN	q9pj6	homo sapien
696	140.5	9.1	429	2	Q96LA6_HUMAN	q96la6	homo sapien
697	140.5	9.1	465	2	Q59E14_DROME	q59e14	drosophila
698	140.5	9.1	476	2	Q4V8J0_RAT	q4v8j0	rattus norv
699	140.5	9.1	551	2	Q8NHN7_HUMAN	q8nhn7	homo sapien
700	140.5	9.0	762	2	Q7ITW8_DROME	q7itw8	drosophila
701	140.5	9.1	773	2	Q61DE4_DROME	q61de4	drosophila
702	140.5	9.1	807	2	Q6NY23_BRARE	q6ny23	brachydanio
703	140.5	1	873	1	FAS2_DROME	fas2	drosophila
704	140.5	9.1	1026	2	CNTN4_HUMAN		homo sapien
705	140.5	9.1	1264	2	O14631_HUMAN	o14631	homo sapien
706	140	9.1	1348	1	VGFR2_COTJA	p52583	coturnix co
707	140.5	9.1	1478	2	Q59H90_HUMAN	q59h90	homo sapien
708	140	9.1	218	2	Q7PJ18_ANOGA	q7pj18	anopheles g
709	140	9.1	299	2	Q7Q0P9_ANOGA	q7q0p9	anopheles g
710	140	9.1	509	2	Q91YK7_MOUSE	q91yk7	mus musculu
711	140	9.1	626	2	Q5E9N1_BOVIN	q5e9n1	bos taurus
712	140	9.1	628	2	Q9M208_BOVIN	q9mz08	bos taurus
713	140	9.1	648	2	Q9EPF1_MOUSE	q9epf1	mus musculu
714	140	9.1	736	2	Q8MYS2_DROME	q8mys2	drosophila
715	140	9.1	774	2	Q9V930_DROME	q9v930	drosophila
716	140	9.1	821	2	Q4S2G2_TETNG	q4s2g2	tetraodon n
717	140	1	890	1	TYRO3_HUMAN	tyro3	homo sapien
718	140	9.1	890	2	Q86VR3_HUMAN	q86vr3	homo sapien
719	140	9.1	951	2	Q59FM9_HUMAN	q59fm9	homo sapien
720	140	9.1	1272	2	Q5GIT3_BRARE	q5git3	brachydanio
721	140	9.1	1702	2	Q4RJ21_TETNG	q4rj21	tetraodon n
722	140	2	2095	2	Q4S8U5_TETNG	q4s8u5	tetraodon n
723	139.5	9.1	324	2	Q8NBY8_HUMAN	q8nby8	homo sapien
724	139.5	9.1	326	2	Q8NC17_HUMAN	q8nc17	homo sapien
725	139.5	9.1	426	1	PSG8_HUMAN	psg8	homo sapien
726	139.5	9.1	939	2	Q9VH85_DROME	q9vh85	drosophila
727	139.5	1	961	1	ROBO4_RAT	robo4	rattus norv
728	139.5	9.1	1193	2	Q9VQW1_DROME	q9vqw1	drosophila
729	139.5	9.1	1320	2	Q96KF5_HUMAN	q96kf5	homo sapien
730	139.5	9.1	1320	2	Q5VV35_HUMAN	q5vv35	homo sapien
731	139.5	9.1	1391	2	Q8N3L4_HUMAN	q8n3l4	homo sapien
732	139.5	9.1	3317	2	Q86YI4_HUMAN	q86yi4	homo sapien
733	139.5	2	7105	2	Q7QJK9_ANOGA	q7qjk9	anopheles g
734	139		17352	2	Q95YM2_PROCL	q95ym2	procambarus
735	139	9.0	292	2	Q6UY47_HUMAN	q6uy47	homo sapien
736	139	9.0	296	2	Q8WMZ2_PIG	q8wmz2	sus scrofa
737	139	9.0	316	2	Q5YCY7_BRARE	q5ycy7	brachydanio
738	139	9.0	368	2	Q5ZJK6_CHICK	q5zjk6	gallus gall
739	139	9.0	416	2	Q7Q1Z7_ANOGA	q7q1z7	anopheles g
740	139	9.0	648	2	Q8R2Y2_MOUSE	q8r2y2	mus musculu
741	139	9.0	723	2	Q86YI4_HUMAN	q86yi4	homo sapien
742	139	9.0	867	2	Q5VZW7_HUMAN	q5vzw7	homo sapien
743	139	9.0	869	1	MUSK_HUMAN	musk	homo sapien
744	139	9.0	875	2	Q5VZW8_HUMAN	q5vzw8	homo sapien
745	139	9.0	922	2	Q90413_BRARE	q90413	brachydanio
746	139	9.0	1020	1	CNTN1_MOUSE	p12960	mus musculu
747	139	9.0	1270	2	Q9U3P2_CAEEL	q9u3p2	caenorhabdi
748	139	9.0	1272	2	Q4JDD5_BRARE	q4jdd5	brachydanio
749	139	9.0	1723	2	Q8CHB2_MOUSE	q8chb2	mus musculu
750	139	9.0	1843	2	Q4SFF7_TETNG	q4sff7	tetraodon n
751	139	9.0	1896	2	Q9IAJ1_XENLA	q9iaj1	xenopus lae
752	139	9.0	4648	2	Q4T3W5_TETNG	q4t3w5	tetraodon n
753	138.5	9.0	288	2	Q9TT70_PIG	q9tt70	sus scrofa
754	138.5	9.0	297	2	Q9BE99_PIG	q9be99	sus scrofa
755	138.5	1	335	1	PSG5_HUMAN	psg5	homo sapien
756	138.5	9.0	345	2	Q6GM08_XENLA	q6gm08	xenopus lae
757	138.5	9.0	419	2	Q96QL5_HUMAN	q96ql5	homo sapien
758	138.5	9.0	467	2	Q4RSP0_MACFA	q4rsp0	macaca fasc
759	138.5	9.0	626	2	Q6DCH3_XENLA	q6dch3	xenopus lae
760	138.5	9.0	815	2	Q80SB9_BRARE	q80sb9	brachydanio
761	138.5	9.0	862	2	Q4SAP3_TETNG	q4sap3	tetraodon n

No			Len	F	Accession		Organism
762	138.5	9.0	204	2	Q6NY23_BRARE	q6ny23	brachydanio
763	138.5	9.0	330	2	Q63241_RAT	q63241	rattus norv
764	138.5	9.0	360	2	Q8MRE6_DROME	q8mre6	drosophila
765	138.5	9.0	366	2	Q8N759_HUMAN	q8n759	homo sapien
766	138.5	9.0	900	2	Q8NFA7_HUMAN	q8nfa7	homo sapien
767	138.5	9.0	940	2	Q95R27_DROME	q95r27	drosophila
768	138.5	9.0	998	2	Q9W4Y6_DROME	q9w4y6	drosophila
769	138.5	9.0	1133	2	Q4T6R9_TETNG	q4t6r9	tetraodon n
770	138.5	9.0	1342	2	Q9GPP6_DROME	q9gpp6	drosophila
771	138.5	9.0	1342	2	Q9VPZ7_DROME	q9vpz7	drosophila
772	138.5	9.0	1879	2	Q7Q0X2_ANOGA	q7q0x2	anopheles g
773	138.5	9.0	1995	2	Q5TNW7_ANOGA	q5tnw7	anopheles g
774	138.5	9.0	2000	2	Q97791_RABIT	q97791	oryctolagus
775	138.5	9.0	4736	2	Q7YT99_MYTGA	q7yt99	mytilus gal
776	138	9.0	204	2	Q7PJY5_ANOGA	q7pjy5	anopheles g
777	138	8.9	345	2	Q63241_RAT	q63241	rattus norv
778	138	8.9	366	2	Q8MRE6_DROME	q8mre6	drosophila
779	138	8.9	438	2	Q8N759_HUMAN	q8n759	homo sapien
780	138	8.9	478	2	Q4RVM0_TETNG	q4rvm0	tetraodon n
781	138	8.9	507	2	Q5K4Q3_PIG	q5k4q3	sus scrofa
782	138	8.9	510	2	Q5E9Z9_BOVIN	q5e9z9	bos taurus
783	138	1	517	1	PVR1_HUMAN	pvr1	homo sapien
784	138	8.9	723	2	Q5SR20_TETNG	q5sr20	tetraodon n
785	138	8.9	727	2	Q6PFK4_BRARE	q6pfk4	brachydanio
786	138	8.9	786	2	TYRO3_MOUSE	tyro3	mus musculu
787	138	8.9	880	2	Q6NZM6_MOUSE	q6nzm6	mus musculu
788	137.5	8.9	880	2	Q4SPY1_TETNG	q4spy1	tetraodon n
789	137.5	8.9	952	2	Q63198_RAT	q63198	rattus norv
790	137.5	8.9	979	2	CNTN1_HUMAN	cntn1	homo sapien
791	137.5	8.9	1049	1	CNTN3_HUMAN	cntn3	homo sapien
792	137.5	8.9	1028	1	Q15229_HUMAN	q15229	homo sapien
793	137.5	8.9	158	2	Q90490_BRARE	q90490	brachydanio
794	137.5	8.9	358	2	Q6UXG0_HUMAN	q6uxg0	homo sapien
795	137.5	8.9	394	2	Q9G176_PIG	q9g176	sus scrofa
796	137.5	1	515	2	Q4TBU1_TETNG	q4tbu1	tetraodon n
797	137.5	8.9	481	2	Q6BE00_XENLA	q6be00	xenopus lae
798	137.5	8.9	489	2	Q4RM24_TETNG	q4rm24	tetraodon n
799	137	8.9	626	1	MAG_MOUSE	mag	mus musculu
800	137.5	1	1237	2	Q610C8_CAEBR	q610c8	caenorhabdi
801	137.5	8.9	2212	2	Q8HNH3_HUMAN	q8hnh3	homo sapien
802	137	8.9	2389	2	Q6BEQ6_CAEEL	q6beq6	caenorhabdi
803	137	8.9	389	2	Q5U3R8_BRARE	q5u3r8	brachydanio
804	137	8.9	481	2	Q5K373_BRARE	q5k373	brachydanio
805	137	8.9	481	2	Q5K374_BRARE	q5k374	brachydanio
806	137	8.9	484	2	Q6BE00_XENLA	q6be00	xenopus lae
807	137	8.9	489	1	PVR1_PIG	pvr1	sus scrofa
808	137	8.9	626	1	MAG_RAT	mag	rattus norv
809	137	8.9	648	2	Q9EPF2_RAT	q9epf2	rattus norv
810	137	8.9	1026	2	Q5I840_PANTR	q5i840	pan troglod
811	137	8.9	1180	2	Q9P2J2_HUMAN	q9p2j2	homo sapien
812	137	8.9	1304	2	NRCAM_HUMAN	nrcam	homo sapien
813	137	8.9	1333	1	VGFR1_MOUSE	vgfr1	mus musculu
814	137	8.9	1333	2	Q23991_DROME	q23991	drosophila
815	137	8.9	1535	2	Q4SPG3_TETNG	q4spg3	tetraodon n
816	137	8.9	1944	2	Q7PH68_ANOGA	q7ph68	anopheles g
817	137	8.9	4071	2	Q7PQG9_ANOGA	q7pqg9	anopheles g
818	137	8.9	4098	2	Q90Z42_CHICK	q90z42	gallus gall
819	136.5	8.9	330	2	Q61353_MOUSE	q61353	mus musculu
820	136.5	8.8	341	1	PCM_BOVIN	p11834	bos taurus
821	136.5	8.8	345	2	Q8VQY0_DROME	q8vqy0	drosophila
822	136.5	8.8	377	1	Q8HXR8_CERAE	q8hxr8	cercopithec
823	136.5	8.8	393	2	Q6NNU3_DROME	q6nnu3	drosophila
824	136.5	8.8	532	2	Q9VLF0_DROME	q9vlf0	drosophila
825	136.5	8.8	532	2	Q4RB52_TETNG	q4rb52	tetraodon n
826	136.5	8.8	557	2	Q8NCE6_HUMAN	q8nce6	homo sapien
827	136.5	8.8	570	2	Q90330_COTCO	q90330	coturnix co
828	136.5	8.8	686	2	Q7PQM9_ANOGA	q7pqm9	anopheles g
829	136.5	8.8	713	2	Q90330_COTCO	q90330	coturnix co
830	136.5	8.8	751	2	Q4KMQ7_HUMAN	q4kmq7	homo sapien
831	136.5	8.8	771	2	Q7QOS6_ANOGA	q7qos6	anopheles g
832	136.5	8.8	956	1	MAMC1_HUMAN	mamc1	homo sapien
833	136.5	8.8	1056	1	CNTN5_BRARE	cntn5	brachydanio
834	136.5	8.8			Q7ZW34	q7zw34	brachydanio

Table — left column (rows 835–907)

#			Len	N	Accession	Accession	Species
835	136.5	8.8	1150	2	Q4SL82_TETNG	Q4sl82	tetraodon n
836	136.5	8.8	1271	2	Q6U714_BRARE	Q6u714	brachydanio
837	136.5	8.8	1280	2	Q90933_CHICK	Q90933	gallus gall
838	136.5	8.8	3375	1	UNC52_CAEEL	O06561	caenorhabdi
839	136	8.8	229	2	Q9TT71_PIG	Q9tt71	sus scrofa
840	136	8.8	230	2	Q9N2I3_PIG	Q9n2i3	sus scrofa
841	136	8.8	510	2	Q96K15_HUMAN	Q96k15	homo sapien
842	136	8.8	510	2	Q96NY8_HUMAN	Q96ny8	homo sapien
843	136	8.8	515	1	PVR1_MOUSE	Q9jkf6	mus musculu
844	136	8.8	515	2	Q6P9M9_MOUSE	Q6p9m9	mus musculu
845	136	8.8	515	2	Q9JKF6_MOUSE	Q9jkf6	mus musculu
846	136	8.8	661	2	O5RJW1_MOUSE	O5rjw1	mus musculu
847	136	8.8	754	2	Q8BZ76_MOUSE	Q8bz76	m mus muscu
848	136	8.8	813	1	PUNC_MOUSE	Q8bqc3	mus musculu
849	136	8.8	814	1	Q8IVU1_HUMAN	Q8ivu1	homo sapien
850	136	8.8	1045	2	Q86T37_HUMAN	Q86t37	homo sapien
851	136	8.8	1045	2	Q5VV36_HUMAN	Q5vv36	homo sapien
852	136	8.8	1320	2	Q86TC9_HUMAN	Q86tc9	homo sapien
853	136	8.8	1376	2	Q5DTJ9_MOUSE	Q5dtj9	mus musculu
854	135.5	8.8	265	2	O02280_CAEEL	O02280	caenorhabdi
855	135.5	8.8	306	2	Q9R1Z9_HUMAN	Q9r1z9	mus musculu
856	135.5	8.8	410	2	Q6R3M2_BOMMO	Q6r3m2	bombyx mori
857	135.5	8.8	442	2	SIGL6_HUMAN	O43699	homo sapien
858	135.5	8.8	466	1	Q4SI43_TETNG	Q4si43	tetraodon n
859	135.5	8.8	782	2	Q5S810_DROME	Q5s810	drosophila
860	135.5	8.8	820	2	Q4SIF9_TETNG	Q4sif9	tetraodon n
861	135.5	8.8	1212	2	TYRO3_RAT	P55146	rattus norv
862	135.5	8.8	1345	2	Q9QVN3_9MURI	Q9qvn3	rattus sp.
863	135.5	8.8	1367	1	Q95428_HUMAN	Q95428	homo sapien
864	135	8.8	1598	2	NRCAM_MOUSE	Q810u4	mus musculu
865	135	8.8	531	2	Q4SW90_TETNG	Q4sw90	tetraodon n
866	135	8.8	659	1	Q4RE88_TETNG	Q4re88	tetraodon n
867	135	8.8	660	2	Q15107_HUMAN	Q15107	homo sapien
868	135	8.8	676	2	Q6MZQ3_HUMAN	Q6mzq3	homo sapien
869	135	8.8	880	1	SIRB1_HUMAN	O00241	homo sapien
870	135	8.8	1154	2	Q4FAT1_BOMMO	Q4fat1	bombyx mori
871	135	8.8	1235	2	Q15228_HUMAN	Q15228	homo sapien
872	135	8.8	1256	2	Q68CR6_HUMAN	Q68cr6	homo sapien
873	135	8.8	1278	2	Q8K1H4_MOUSE	Q8k1h4	mus musculu
874	135	8.8	3084	2	O55095_MOUSE	O55095	mus musculu
875	134.5	8.8	180	2	NTRK2_CHICK	Q91987	gallus gall
876	134.5	8.8	322	2	Q7PME2_ANOGA	Q7pme2	anopheles g
877	134.5	8.8	370	2	MAMC1_MOUSE	P60755	mus musculu
878	134.5	8.8	398	1	CNTN3_MOUSE	Q07409	mus musculu
879	134.5	8.8	410	2	Q5IS85_9PRIM	Q5is85	saimiri bol
880	134.5	8.8	411	2	O18465_HIRME	O18465	hirudo medi
881	134.5	8.8	419	2	Q8WZ51_HUMAN	Q8wz51	homo sapien
882	134.5	8.8	688	2	Q7YRF6_CANFA	Q7yrf6	canis famil
883	134.5	8.8	688	1	O02870_CHICK	O02870	gallus gall
884	134.5	8.8	818	2	Q5WRG1_SHEEP	Q5wrg1	ovis aries
885	134.5	8.8	904	2	Q8B0I4_HUMAN	Q8b0i4	homo sapien
886	134.5	8.8	949	1	O8JFU3_BRARE	O8jfu3	brachydanio
887	134.5	8.8	1028	2	Q7SY58_BRARE	Q7sy58	brachydanio
888	134.5	8.8	1180	2	Q63093_RAT	Q63093	rattus norv
889	134.5	8.8	1880	2	O26475_SCHAM	O26475	schistocerc
890	134.5	8.8	2154	2	LU_HUMAN	P50895	homo sapien
891	134	8.7	2200	1	P50895	P50895	homo sapien
892	134	8.7	308	2	Q26261	Q26261	caenorhabdi
893	134	8.7	334	2	O26475	O26475	homo sapien
894	134	8.7	344	2	O26475	O26475	brachydanio
895	134	8.7	351	2	Q7SY58_BRARE	Q7sy58	brachydanio
896	134	8.7	458	2	Q63093_RAT	Q63093	rattus norv
897	134	8.7	484	1	O26475_SCHAM	O26475	schistocerc
898	134	8.7	628	1	LU_HUMAN	P50895	homo sapien
899	134	8.7	919	1	P50895	P50895	homo sapien
900	134	8.7	941	1	Q5J1R9_BRARE	Q5j1r9	brachydanio
901	134	8.7	1044	1	Q96IW3_HUMAN	Q96iw3	homo sapien
902	134	8.7	1077	2	Q5WN88_CAEBR	Q5wn88	caenorhabdi
903	134	8.7	2095	2	Q4RYE5_TETNG	Q4rye5	tetraodon n
904	133.5	8.6	241	2	Q4T4Z6_TETNG	Q4t4z6	tetraodon n
905	133.5	8.6	308	1	O8UUG3_ICTPU	O8uug3	ictalurus p
906	133.5	8.6	330	1	EMB_MOUSE	P21995	mus musculu
907	133.5	8.6	331	2	O63239_RAT	O63239	rattus norv

Table — middle column (rows 908–980)

#			Len	N	Accession	Accession	Species
908	133.5	8.6	333	1	CD2226_MOUSE	cd2226	mus musculu
909	133.5	8.6	333	1	Q5DW69_MOUSE	q5dw69	mus musculu
910	133.5	8.6	410	2	Q6R3M0_BOMMO	q6r3m0	bombyx mori
911	133.5	8.6	410	2	Q7YZA7_BOMMO	q7yza7	bombyx mori
912	133.5	8.6	419	1	PSG1_HUMAN	p11464	homo sapien
913	133.5	8.6	426	2	Q61CR4_HUMAN	q61cr4	homo sapien
914	133.5	8.6	428	2	Q9BRW2_HUMAN	q9brw2	homo sapien
915	133.5	8.6	501	2	Q6G147_BOVIN	q6g147	bos taurus
916	133.5	8.6	618	1	Q49HD7_TETNG	q49hd7	tetraodon n
917	133.5	8.6	626	2	Q53HA1_HUMAN	q53ha1	homo sapien
918	133.5	8.6	632	2	Q6ZRK5_HUMAN	q6zrk5	homo sapien
919	133.5	8.6	729	2	Q63827_RAT	q63827	rattus norv
920	133.5	8.6	763	1	Q5YM9_HALRO	q5ym9	halocynthia
921	133.5	8.6	949	1	P60756_RAT	p60756	rattus norv
922	133.5	8.6	949	1	Q4SL83_TETNG	q4sl83	tetraodon n
923	133.5	8.6	1250	2	Q8TDY8_HUMAN	q8tdy8	homo sapien
924	133.5	8.6	1250	2	O88971_MOUSE	o88971	mus musculu
925	133.5	8.6	223	2	Q7QCH7_ANOGA	q7qch7	anopheles g
926	133.5	8.6	239	2	Q4SPD7_TETNG	q4spd7	tetraodon n
927	133	8.6	337	2	Q6DFY2_MOUSE	q6dfy2	mus musculu
928	133	8.6	354	2	Q5R645_PONPY	q5r645	pongo pygma
929	133	8.6	428	1	Q60XJ4_HUMAN	q60xj4	homo sapien
930	133	8.6	477	2	P79757_CHICK	p79757	gallus gall
931	133	8.6	508	2	Q961K8_DROME	q961k8	drosophila
932	133	8.6	508	2	Q9VZZ4_DROME	q9vzz4	drosophila
933	133	8.6	508	1	Q7PT04_ANOGA	q7pt04	anopheles g
934	133	8.6	1311	2	Q15108_HUMAN	q15108	homo sapien
935	133	8.6	1527	2	Q15106_HUMAN	q15106	homo sapien
936	132.5	8.6	189	2	Q15108_HUMAN	q15108	homo sapien
937	132.5	8.6	278	2	Q51SM6_MACFA	q51sm6	macaca fasc
938	132.5	8.6	302	2	Q5ISA8_9PRIM	q5isa8	saimiri bol
939	132.5	8.6	319	1	OPCM_HUMAN	q14982	homo sapien
940	132.5	8.6	345	1	OPCM_PANTR	p32736	pan troglod
941	132.5	8.6	345	2	Q5I861_RAT	q5i861	rattus norv
942	132.5	8.6	345	1	Q68EV1_XENLA	q68ev1	xenopus lae
943	132.5	8.6	336	2	Q4RRS5_TETNG	q4rrs5	tetraodon n
944	132.5	8.6	508	2	ROBO4_DROME	q9vn4	drosophila
945	132.5	8.6	822	1	Q6NR54_DROME	q6nr54	drosophila
946	132.5	8.6	1012	2	ROBO4_RAT	q6p1m7	rattus norv
947	132.5	8.6	1173	2	Q4RRS5_TETNG	q4rrs5	tetraodon n
948	132.5	8.6	1278	2	Q68EV1_XENLA	q68ev1	xenopus lae
949	132.5	8.6	308	1	Q6BEV1_XENLA	q6bev1	xenopus bol
950	132.5	8.6	345	1	Q51SA8_9PRIM	q51sa8	saimiri bol
951	132.5	8.6	345	1	OPCM_HUMAN	q14982	homo sapien
952	132.5	8.6	405	1	OPCM_PANTR	p32736	pan troglod
953	132.5	8.6	474	1	Q5I861_RAT	q5i861	rattus norv
954	132	8.6	484	2	Q7PRJ5_ANOGA	q7prj5	anopheles g
955	132	8.6	484	2	Q5FV48_FUGRU	q5fv48	fugu rubrip
956	132	8.6	508	2	Q5G811_XENTR	q5g811	xenopus tro
957	132	8.6	627	2	Q8BJA5_MOUSE	q8bja5	mus musculu
958	132	8.6	707	2	Q5RDU0_PONPY	q5rdu0	pongo pygma
959	132	8.6	743	1	Q8BJ23_MOUSE	q8bj23	mus musculu
960	132	8.6	947	1	Q6P1M7_HUMAN	q6p1m7	homo sapien
961	132	8.6	1018	1	CNTN1_BOVIN	q28106	bos taurus
962	132	8.6	1018	1	CNTN1_HUMAN	q12860	homo sapien
963	132	8.6	1019	2	Q9QVN4_9MURI	q9qvn4	rattus sp.
964	132	8.6	1166	2	Q6PW35_RAT	q6pw35	rattus norv
965	132	8.6	1194	2	Q6PW35_RAT	q6pw35	rattus norv
966	132	8.6	1197	2	Q6PW38_RAT	q6pw38	rattus norv
967	132	8.6	1198	2	Q6PW37_RAT	q6pw37	rattus norv
968	132	8.6	1206	2	Q6PW36_RAT	q6pw36	rattus norv
969	132	8.6	1209	2	Q6PW39_RAT	q6pw39	rattus norv
970	132	8.6	1214	2	NRCAM_RAT	p976e6	rattus norv
971	132	8.6	1299	2	Q6PW34_RAT	q6pw34	rattus norv
972	132	8.6	263	1	Q7TPW5_MOUSE	q7tpw5	mus musculu
973	131.5	8.5	417	1	PVR_MOUSE	p15151	mus musculu
974	131.5	8.5	419	1	PSG4_HUMAN	o00888	homo sapien
975	131.5	8.5	731	2	Q6CFK8_MOUSE	q6cfk8	mus musculu
976	131.5	8.5	733	2	O60830_MOUSE	o60830	mus musculu
977	131.5	8.5	764	2	Q5RDC2_PONPY	q5rdc2	pongo pygma
978	131.5	8.5	764	1	Q5RA58_PONPY	q5ra58	pongo pygma
979	131.5	8.5	789	1	KIRR1_RAT	q6x936	rattus norv
980	131.5	8.5	820	2	Q8CIM9_MOUSE	q8cim9	mus musculu

Table — right column (accessions)

Accession	Accession	Species
Q8K4E0_MOUSE	q8k4e0	mus musculu
Q5DW69_MOUSE	q5dw69	mus musculu
Q6R3M0_BOMMO	q6r3m0	bombyx mori
Q7YZA7_BOMMO	q7yza7	bombyx mori
P11464_HUMAN	p11464	homo sapien
Q61CR4_HUMAN	q61cr4	homo sapien
Q9BRW2_HUMAN	q9brw2	homo sapien
Q6G147_BOVIN	q6g147	bos taurus
Q49HD7_TETNG	q49hd7	tetraodon n
Q53HA1_HUMAN	q53ha1	homo sapien
Q6ZRK5_HUMAN	q6zrk5	homo sapien
Q63827_RAT	q63827	rattus norv
Q5YM9_HALRO	q5ym9	halocynthia
P60756_RAT	p60756	rattus norv
Q4SL83_TETNG	q4sl83	tetraodon n
Q8TDY8_HUMAN	q8tdy8	homo sapien
O88971_MOUSE	o88971	mus musculu
Q7QCH7_ANOGA	q7qch7	anopheles g
Q4SPD7_TETNG	q4spd7	tetraodon n
Q6DFY2_MOUSE	q6dfy2	mus musculu
Q5R645_PONPY	q5r645	pongo pygma
Q60XJ4_HUMAN	q60xj4	homo sapien
P79757_CHICK	p79757	gallus gall
Q961K8_DROME	q961k8	drosophila
Q9VZZ4_DROME	q9vzz4	drosophila
Q7PT04_ANOGA	q7pt04	anopheles g
Q15108_HUMAN	q15108	homo sapien
Q15106_HUMAN	q15106	homo sapien
Q15108_HUMAN	q15108	homo sapien
Q51SM6_MACFA	q51sm6	macaca fasc
Q5ISA8_9PRIM	q5isa8	saimiri bol
OPCM_HUMAN	q14982	homo sapien
OPCM_PANTR	p32736	pan troglod
Q5I861_RAT	q5i861	rattus norv
Q68EV1_XENLA	q68ev1	xenopus lae
Q4RRS5_TETNG	q4rrs5	tetraodon n
ROBO4_DROME	q9vn4	drosophila
Q6NR54_DROME	q6nr54	drosophila
FGFR1_RAT	q04589	rattus norv
Q8AXY6_HUMAN	q8axy6	homo sapien
MUSK_CHICK	q6p1m7	gallus gall
Q9QVN4_9MURI	q9qvn4	mus musculu
CNTN1_HUMAN	q12860	homo sapien
Q6P1M7_HUMAN	q6p1m7	homo sapien
Q6PW35_RAT	q6pw35	rattus norv
Q6PW35_RAT	q6pw35	rattus norv
Q6PW37_RAT	q6pw37	rattus norv
Q6PW38_RAT	q6pw38	rattus norv
Q6PW36_RAT	q6pw36	rattus norv
Q6PW39_RAT	q6pw39	rattus norv
NRCAM_RAT	p976e6	rattus norv
Q6PW34_RAT	q6pw34	rattus norv
Q7TPW5_MOUSE	q7tpw5	mus musculu
PVR_MOUSE	p15151	mus musculu
PSG4_HUMAN	o00888	homo sapien
Q6CFK8_MOUSE	q6cfk8	mus musculu
O60830_MOUSE	o60830	mus musculu
Q5RDC2_PONPY	q5rdc2	pongo pygma
Q5RA58_PONPY	q5ra58	pongo pygma
Q6X936_RAT	q6x936	rattus norv
Q8CIM9_MOUSE	q8cim9	mus musculu

#			Len	N	Code	Accession	Organism
981	131.5	8.5	822	1	FGFR1_MOUSE	P16092	mus musculu
982	131.5	8.5	822	2	Q60818	Q60818	mus musculu
983	131.5	8.5	1047	2	Q4RGC7_TETNG	Q4rgc7	tetraodon n
984	131.5	8.5	1266	1	NGCA_CHICK	Q03696	gallus gall
985	131.5	8.5	1335	2	Q61OC7_CAEBR	Q61oc7	caenorhabdi
986	131.5	8.5	2029	1	P16621_DROME	P16621	drosophila
987	131.5	8.4	2057	2	LAR_DROME	Q4t2n4	tetraodon n
988	131	8.5	226	2	Q4T2N4_TETNG	Q4t2n4	tetraodon n
989	131	8.5	321	2	Q8N440_HUMAN	Q8n440	homo sapien
990	131	8.5	340	2	Q5WRG0_SHEEP	Q5wrg0	ovis aries
991	131	8.5	352	1	Q61349_MOUSE	Q61349	mus musculu
992	131	8.5	352	2	NEGR1_HUMAN	Q7z3b1	homo sapien
993	131	8.5	354	2	Q7Z3B1_HUMAN	Q7z3b1	homo sapien
994	131	8.5	354	2	Q5VT21_HUMAN	Q5vt21	homo sapien
995	131	8.5	362	2	Q5R412_PONPY	Q5r412	pongo pygma
996	131	8.5	412	2	Q9JHQ1_RAT	Q9jhq1	rattus norv
997	131	8.5	412	2	Q5U334_RAT	Q5u334	rattus norv
998	131	8.5	412	2	Q63611_RAT	Q63611	rattus norv
999	131	8.5	463	2	Q9R1E1_RAT	Q9r1e1	rattus norv
1000	131	8.5	500	2	Q4VAH7_MOUSE	Q4vah7	mus musculu
1001	131	8.5	500	2	Q9XZB7_DROME	Q9xzb7	drosophila
1002	131	8.5	501	2	Q9W260_DROME	Q9w260	drosophila
1003	131	8.5	636	2	Q4SZC5_TETNG	Q4szc5	tetraodon n
1004	131	8.5	831	2	Q22040_CAEEL	Q22040	caenorhabdi
1005	131	8.5	1012	2	Q7ISY9_CHICK	Q71sy9	gallus gall
1006	131	8.5	1276	2	Q95L3_BRARE	Q95l3	brachydanio
1007	130.5	8.5	1944	2	Q90X22_BRARE	Q90x22	brachydanio
1008	130.5	8.5	173	2	Q69SL3_BRARE	Q69513	brachydanio
1009	130.5	8.5	238	2	O7PSS8_ANOGA	O7pss8	anopheles g
1010	130.5	8.5	313	2	Q20339_CAEEL	Q20339	caenorhabdi
1011	130.5	8.5	383	2	Q9U964_GEOCY	Q9u964	geodia cydo
1012	130.5	8.5	393	1	O18431_GEOCY	O18431	geodia cydo
1013	130.5	8.5	424	2	I11R2_CERAE	I11r2	cercopithec
1014	130.5	8.5	435	1	PSG10_HUMAN	Q15235	homo sapien
1015	130.5	8.5	549	2	PSG6_HUMAN	O00889	homo sapien
1016	130.5	8.5	562	2	Q9U965_GEOCY	Q9u965	geodia cydo
1017	130.5	8.5	593	2	Q6YNR7_BRARE	Q6ynr7	brachydanio
1018	130.5	8.5	757	1	Q5W0F9_HUMAN	Q5w0f9	homo sapien
1019	130.5	8.5	757	2	KIRR1_HUMAN	Q96j84	homo sapien
1020	130.5	8.5	814	2	Q5W0F8_HUMAN	Q5w0f8	homo sapien
1021	130.5	8.5	877	2	Q9VNP2_DROME	Q9vnp2	drosophila
1022	130.5	8.5	1011	2	Q9GSH3_HALRO	Q9gsh3	halocynthia
1023	130.5	8.5	1033	2	O24273_DROME	O24273	drosophila
1024	130	8.5	166	2	Q4SBZ7_TETNG	Q4sbz7	tetraodon n
1025	130	8.5	229	2	Q15226_HUMAN	Q15226	homo sapien
1026	130	8.5	270	2	Q9R121_RAT	Q9r121	rattus norv
1027	130	8.5	337	2	Q8BTP3_MOUSE	Q8btp3	mus musculu
1028	130	8.5	509	2	Q90288_BRARE	Q90288	brachydanio
1029	130	8.5	529	1	P6P618_MOUSE	P6p618	mus musculu
1030	130	8.5	888	2	FGRL1_MOUSE	Q91v87	mus musculu
1031	130	8.5	1019	2	Q4VBK2_BRARE	Q4vbk2	brachydanio
1032	130	8.5	1106	2	Q9Y6L9_HUMAN	Q9y619	homo sapien
1033	130	8.5	1228	2	Q8WX93_HUMAN	Q8wx93	homo sapien
1034	130	8.5	1235	2	Q8MRA3_DROME	Q8mra3	drosophila
1035	130	8.5	1235	2	Q9V787_DROME	Q9v787	drosophila
1036	130	8.5	1252	2	Q86BD5_DROME	Q86bd5	drosophila
1037	130	8.5	1253	2	Q9EQS8_MOUSE	Q9eqs8	mus musculu
1038	130	8.5	1409	2	Q801M2_BRARE	Q801m2	brachydanio
1039	130	8.5	1409	2	Q8J127_BRARE	Q8j127	brachydanio
1040	130	8.5	1428	2	Q8AY67_BRARE	Q8ay67	brachydanio
1041	130	8.5	2200	1	LAR_CAEEL	Q9bmn8	caenorhabdi
1042	129.5	8.5	151	2	Q4THV8_TETNG	Q4thv8	tetraodon n
1043	129.5	8.5	275	2	Q6PH44_BRARE	Q6ph44	brachydanio
1044	129.5	8.5	306	1	CD80_MOUSE	O00609	mus musculu
1045	129.5	8.5	306	2	Q549R2_MOUSE	Q549r2	mus musculu
1046	129.5	8.5	323	2	Q5U198_DROME	Q5u198	drosophila
1047	129.5	8.5	338	2	Q5R7T4_PONPY	Q5r7t4	pongo pygma
1048	129.5	8.5	338	2	Q7Z3W6_HUMAN	Q7z3w6	homo sapien
1049	129.5	8.4	398	2	Q7Z3B9_HUMAN	Q7z3b9	homo sapien
1050	129.5	8.4	403	2	Q9N2H5_HORSE	Q9n2h5	equus cabal
1051	129.5	8.4	409	2	Q4SFV2_TETNG	Q4sfv2	tetraodon n
1052	129.5	8.4	438	2	Q9JLB7_MOUSE	Q9jlb7	mus musculu
1053	129.5	8.4	466	2	Q4VWT2_9PIPI	Q4vwt2	xenopus sp.

#			Len	N	Code	Accession	Organism
1054	129.5	8.4	510	2	Q9JLB8_MOUSE	Q9jlb8	mus musculu
1055	129.5	8.4	731	2	Q5BJG2_HUMAN	Q5bjg2	homo sapien
1056	129.5	8.4	740	1	PECA1_PIG	P...	sus scrofa
1057	129.5	8.4	750	2	Q646H5_CAEEL	Q646h5	caenorhabdi
1058	129.5	8.4	785	2	Q5XG39_XENLA	Q5xg39	xenopus lae
1059	129.5	8.4	797	2	Q52V40_BRAFL	Q52v40	branchiosto
1060	129.5	8.4	814	2	Q59H40_HUMAN	Q59h40	homo sapien
1061	129.5	8.4	822	1	FGFR2_HUMAN	P11362	homo sapien
1062	129.5	8.4	822	2	Q91288_PLEWA	Q91288	pleurodeles
1063	129.5	8.4	874	2	Q9YI66_BRARE	Q9yi66	brachydanio
1064	129.5	8.4	1073	2	Q9TXI8_CAEEL	Q9txi8	caenorhabdi
1065	129.5	8.4	1073	2	Q9W1T8_DROME	Q9w1t8	drosophila
1066	129.5	8.4	1098	2	Q961D6_DROME	Q961d6	drosophila
1067	129.5	8.4	1343	2	VGFR2_RAT	Q08775	rattus norv
1068	129.5	8.4	19066	2	Q801W6_BRARE	Q801w6	m mus muscu
1069	129	8.4	181	2	Q9CWD9_MOUSE	Q9cwd9	mus musculu
1070	129	8.4	266	2	Q566X2_BRARE	Q566x2	brachydanio
1071	128	8.4	336	1	CD226_MACMU	O18906	macaca mula
1072	129	8.4	393	2	Q95727_HUMAN	Q95727	homo sapien
1073	129	8.4	459	2	Q86X91_HUMAN	Q86x91	homo sapien
1074	129	8.4	459	2	Q91AR9_CHICK	Q91ar9	gallus gall
1075	129	8.4	542	2	Q801V8_BRARE	Q801v8	homo sapien
1076	129	8.4	802	2	Q801V8_BRARE	Q801v8	brachydanio
1077	129	8.4	816	2	Q95M13_BOVIN	Q95m13	homo sapien
1078	129	8.4	1014	2	Q8NHN5_HUMAN	Q8nhn5	homo sapien
1079	129	8.4	1197	2	Q95M13_BOVIN	Q95m13	bos taurus
1080	129	8.4	1357	2	Q91285_PLEWA	Q91285	homo sapien
1081	129	8.4	1357	2	Q8NPA6_HUMAN	Q8npa6	brachydanio
1082	129	8.4	1427	2	Q4RVM1_TETNG	Q4rvm1	brachydanio
1083	129	8.4	2164	2	Q5MD89_BRARE	Q5md89	xenopus lae
1084	129	8.4	3100	2	Q5GIT2_BRARE	Q5git2	gallus gall
1085	129	8.4	4650	2	Q91562_XENLA	Q91562	homo sapien
1086	129	8.4	4650	2	Q9IAR9_CHICK	Q9iar9	homo sapien
1087	129	8.4	5505	2	Q7KYN5_HUMAN	Q7kyn5	tetraodon n
1088	129	8.4	5505	2	Q15598_HUMAN	Q15598	brachydanio
1089	128.5	8.4	18412	2	Q4RU89_TETNG	Q4ru89	brachydanio
1090	128.5	8.4	341	2	Q7ZZ61_BRARE	Q7zz61	mus musculu
1091	128.5	8.4	341	2	Q4T419_TETNG	Q4t419	homo sapien
1092	128.5	8.4	322	2	Q96I69_HUMAN	Q96i69	brachydanio
1093	128.5	8.4	233	1	Q9Z0J8_MOUSE	Q9z0j8	rattus norv
1094	128.5	8.4	348	2	Q503N3_BRARE	Q503n3	h basigin p
1095	128.5	8.3	385	1	BASI_HUMAN	P35613	homo sapien
1096	128.5	8.3	398	2	Q5XI11_HUMAN	Q5xi11	sania cynth
1097	128.5	8.3	413	2	Q4H1G8_SAMCR	Q4h1g8	homo sapien
1098	128.5	8.3	419	2	Q6P520_HUMAN	Q6p520	mus musculu
1099	128.5	8.3	549	1	Q9JLB9_MOUSE	Q9jlb9	rattus norv
1100	128.5	8.3	574	2	Q58EG3_BRARE	Q58eg3	brachydanio
1101	128.5	8.3	797	2	Q52V39_BRAFL	Q52v39	branchiosto
1102	128.5	8.3	1343	2	Q5PQU0_RAT	Q5pqu0	brachydanio
1103	128.5	8.3	2935	2	Q7Z1Y4_DROME	Q7z1y4	drosophila
1104	128.5	8.3	2935	2	Q9W053_DROME	Q9w053	drosophila
1105	128	8.3	243	2	Q611Y6_CAEBR	Q611y6	caenorhabdi
1106	128	8.3	331	2	Q91B01_9PERC	Q91b01	sphoeroides
1107	128	8.3	393	2	Q6IRX2_HUMAN	Q6irx2	homo sapien
1108	128	8.3	422	2	Q96PJ3_HUMAN	Q96pj3	mus musculu
1109	128	8.3	423	2	Q8BU57_MOUSE	Q8bu57	mus musculu
1110	128	8.3	506	2	SHPS1_BOVIN	O46631	bos taurus
1111	128	8.3	542	2	Q5U5W7_MOUSE	Q5u5w7	mus musculu
1112	128	8.3	707	2	Q9TT07_CANFA	Q9tt07	canis famil
1113	128	8.3	739	2	Q60NV9_CAEBR	Q60nv9	caenorhabdi
1114	128	8.3	823	1	CEK3_CHICK	P18461	gallus gall
1115	128	8.3	1032	2	Q8AXZ4_BRARE	Q8axz4	brachydanio
1116	128	8.3	1253	2	CNT1A_TETNG	Q4SCT8	tetraodon n
1117	127.5	8.3	1994	2	Q6ZPP2_MOUSE	Q6zpp2	mus musculu
1118	127.5	8.3	2176	2	Q6V4S5_MOUSE	Q6v4s5	mus musculu
1119	127.5	8.3	276	2	Q8OT70_MOUSE	Q8ot70	homo sapien
1120	127.5	8.3	276	2	Q5MKL4_HUMAN	Q5mkl4	anopheles g
1121	127.5	8.3	323	2	Q7QBA7_ANOGA	Q7qba7	homo sapien
1122	127.5	8.3	348	2	Q8NF28_HUMAN	Q8nf28	mus musculu
1123	127.5	8.3	388	2	NEGR1_MOUSE	Q80z24	homo sapien
1124	127.5	8.3	422	1	Q8WR61_LYMDI	Q8wr61	equus cabal
1125	127.5	8.3	487	1	FGRL1_CHICK	Q7t2h2	tetraodon n
1126	127.5	8.3	898	1	FAS2_SCHAM	P22648	brachydanio

No.			Len	N	Name	Accession	Organism
1127	127.5	8.3	1106	1	PGFRB_HUMAN	P09619	homo sapien
1128	127.5	8.3	1197	2	L1CA1_BRARE	Q90478	brachydanio
1129	127.5	8.3	1269	1	Q6U7I5_BRARE	Q6u7i5	brachydanio
1130	127.5	8.3	1304	2	Q9VBE5_DROME	Q9vbe5	drosophila
1131	127	8.2	183	2	Q8NHN6_HUMAN	Q8nhn6	homo sapien
1132	127	8.2	271	2	Q4S7L7_TETNG	Q4s7l7	tetraodon n
1133	127	8.2	276	2	Q4SF97_TETNG	Q4sf97	tetraodon n
1134	127	8.2	353	2	Q63242_RAT	Q63242	rattus norv
1135	127	8.2	413	2	Q9VAR6_DROME	Q9var6	drosophila
1136	127	8.2	416	1	RAGE_BOVIN	Q28173	bos taurus
1137	127	8.2	459	2	Q4RS41_TETNG	Q4rs41	tetraodon n
1138	127	8.2	461	2	Q4RFF6_TETNG	Q4rff6	tetraodon n
1139	127	8.2	515	2	Q96RE0_HUMAN	Q96re0	homo sapien
1140	127	8.2	515	2	Q96PJ5_HUMAN	Q96pj5	homo sapien
1141	127	8.2	523	2	Q80ZE2_MOUSE	Q80ze2	mus musculu
1142	127	8.2	569	1	SIGL5_MOUSE	Q92og3	mus musculu
1143	127	8.2	686	1	IRPL2_HUMAN	Q9np60	h x-linked
1144	127	8.2	686	2	CEAM3_RAT	Q63111	rattus norv
1145	127	8.2	709	2	Q5H9L9_HUMAN	Q5h9l9	homo sapien
1146	127	8.2	800	2	Q918X3_BRARE	Q918x3	brachydanio
1147	127	8.2	810	2	Q9PS96_XENLA	Q9ps96	xenopus lae
1148	127	8.2	873	2	Q98949_CHICK	Q98949	gallus gall
1149	127	8.2	1009	2	Q93250_XENLA	Q93250	xenopus lae
1150	127	8.2	1193	2	Q4RHM4_TETNG	Q4rhm4	tetraodon n
1151	127	8.2	4816	2	Q8T103_BOMMO	Q8t103	bombyx mori
1152	126.5	8.2	272	2	Q9VAV8_DROME	Q9vav8	drosophila
1153	126.5	8.2	311	2	Q6DN73_HUMAN	Q6dn73	homo sapien
1154	126.5	8.2	446	2	Q4S1B2_TETNG	Q4s1b2	tetraodon n
1155	126.5	8.2	389	2	BASI_MOUSE	P18572	mus musculu
1156	126.5	8.2	513	2	Q9D6N4_MOUSE	Q9d6n4	mus musculu
1157	126.5	8.2	820	2	Q53H63_HUMAN	Q53h63	homo sapien
1158	126.5	8.2	824	2	Q90749_CHICK	Q90749	gallus gall
1159	126.5	8.2	986	2	Q8UVR9_FUGRU	Q8uvr9	fugu rubrip
1160	126.5	8.2	1232	2	Q90284_CARAU	Q90284	carassius a
1161	126.5	8.2	1238	2	Q62AJ4_CAEBR	Q62aj4	caenorhabdi
1162	126.5	8.2	1445	2	Q63155_RAT	Q63155	rattus norv
1163	126.5	8.2	1447	1	DCC_HUMAN	P43146	homo sapien
1164	126	8.2	270	2	Q4FZV9_XENLA	Q4fzv9	xenopus lae
1165	126	8.2	275	2	Q55107_MOUSE	Q55107	mus musculu
1166	126	8.2	332	2	Q9VAV8_DROME	Q9vav8	drosophila
1167	126	8.2	386	2	Q4S1B2_TETNG	Q4s1b2	tetraodon n
1168	126	8.2	389	2	Q62664_RAT	Q62664	rattus norv
1169	126	8.2	475	1	FGRL1_RAT	P97527	rattus norv
1170	126	8.2	529	1	FGRL1_RAT	Q7tqm3	rattus norv
1171	126	8.2	529	2	Q7TQM3_RAT	Q7tqm3	rattus norv
1172	126	8.2	673	1	Q4V8P8_RAT	Q4v8p8	rattus norv
1173	126	8.2	708	2	Q6MZW2_HUMAN	Q6mzw2	homo sapien
1174	126	8.2	881	2	KIRR2_HUMAN	Q6uwl6	homo sapien
1175	126	8.2	941	2	Q95SM2_CAEEL	Q95sm2	caenorhabdi
1176	126	8.2	1099	2	Q4SMD8_TETNG	Q4smd8	tetraodon n
1177	126	8.2	1252	1	CNTN5_MOUSE	P97527	mus musculu
1178	126	8.2	1292	2	Q9JLI1_MOUSE	Q9jli1	mus musculu
1179	126	8.2	1327	2	Q4RHM3_TETNG	Q4rhm3	tetraodon n
1180	126	8.2	1356	2	VGFR2_HUMAN	P35968	homo sapien
1181	126	8.2	1451	2	Q59EB0_HUMAN	Q59eb0	homo sapien
1182	126	8.2	4796	2	Q9NL88_DROME	Q9nl88	drosophila
1183	126	8.2	4796	2	Q9W0S5_DROME	Q9w0s5	drosophila
1184	125.5	8.1	140	2	Q4SL88_TETNG	Q4sl88	tetraodon n
1185	125.5	8.1	337	2	Q8UV29_BRARE	Q8uv29	brachydanio
1186	125.5	8.1	337	2	Q90ZB7_BRARE	Q90zb7	brachydanio
1187	125.5	8.1	398	1	I1R2_HUMAN	P27930	homo sapien
1188	125.5	8.1	400	2	Q8HY16_CEBAP	Q8hy16	cebus apell
1189	125.5	8.1	419	2	PSG7_HUMAN	Q13046	homo sapien
1190	125.5	8.1	439	2	Q57J49_CHICK	Q57j49	gallus gall
1191	125.5	8.1	460	2	Q8MJZ4_PANTR	Q8mjz4	pan troglod
1192	125.5	8.1	606	2	Q9ESS7_MOUSE	Q9ess7	mus musculu
1193	125.5	8.1	683	2	Q5TTJ6_ANOGA	Q5ttj6	anopheles g
1194	125.5	8.1	687	2	Q9JJ08_RAT	Q9jj08	rattus norv
1195	125.5	8.1	737	2	Q965M3_CAEEL	Q965m3	caenorhabdi
1196	125.5	8.1	743	2	Q6R6B2_9CAUD	Q6r6b2	vibrio phag
1197	125.5	8.1	747	2	Q4H3K6_CIOIN	Q4h3k6	ciona intes
1198	125.5	8.1	789	2	KIRR1_MOUSE	O80w68	mus musculu
1199	125.5	8.1	821	1	FGFR2_HUMAN	P21802	homo sapien

No.			Len	N	Name	Accession	Organism
1200	125.5	8.1	1028	1	CNTN3_RAT	O62682	rattus norv
1201	125.5	8.1	1055	2	Q61YY0_CAEBR	Q61yy0	caenorhabdi
1202	125.5	8.1	1263	2	Q723B7_HUMAN	Q723b7	homo sapien
1203	125.5	8.1	1284	1	NRCAM_CHICK	P35331	gallus gall
1204	125.5	8.1	234	2	Q5C294_HUMAN	Q5c294	homo sapien
1205	125.5	8.1	235	2	Q75296_HUMAN	O75296	homo sapien
1206	125	8.1	260	2	Q9QW80_9MURI	Q9qw80	mus sp. fib
1207	125	8.1	287	2	Q9QW80_9MURI	Q9qw80	mus musculu
1208	125	8.1	360	1	Q8BJ10_MOUSE	Q8bj10	mus musculu
1209	125	8.1	376	2	Q9QW78_MOUSE	Q9qw78	mus sp. fib
1210	125	8.1	403	2	Q8HY15_LEMCA	Q8hy15	lemur catta
1211	125	8.1	495	2	Q9JH17_RAT	Q9jh17	rattus norv
1212	125	8.1	530	1	PVR2_MOUSE	P32507	mus musculu
1213	125	8.1	603	2	Q80XJ5_MOUSE	Q80xj5	mus musculu
1214	125	8.1	626	2	Q4SLP0_TETNG	Q4slp0	tetraodon n
1215	125	8.1	709	2	Q4SMS6_TETNG	Q4sms6	tetraodon n
1216	125	8.1	766	2	Q4KLZ7_RAT	Q4klz7	rattus norv
1217	125	8.1	775	2	Q7Q0S7_ANOGA	Q7q0s7	anopheles g
1218	125	8.1	937	2	Q97754_RABIT	Q97754	oryctolagus
1219	125	8.1	1072	2	Q5WN68_CAEBR	Q5wn68	caenorhabdi
1220	125	8.1	1802	1	Q8T104_BOMMO	Q8t104	bombyx mori
1221	125	8.1	4001	2	Q28633_RABIT	Q28633	oryctolagus
1222	125	8.1	235	2	Q2N2P7_DROME	Q2n2p7	drosophila
1223	124.5	8.1	235	1	Q9N0T0_CANFA	Q9n0t0	canis famil
1224	124.5	8.1	284	2	Q9TQS8_CANFA	Q9tqs8	canis famil
1225	124.5	8.1	304	2	Q9GL33_BOVIN	Q9gl33	bos taurus
1226	124.5	8.1	325	2	Q9TQX1_CANFA	Q9tqx1	canis famil
1227	124.5	8.1	327	1	Q8UWL3_ICTPU	Q8uwl3	ictalurus p
1228	124.5	8.1	359	2	EMB_HUMAN	O6pcb8	homo sapien
1229	124.5	8.1	413	2	Q4KLE4_XENLA	Q4kle4	xenopus lae
1230	124.5	8.1	698	2	Q26438_HYACE	Q26438	hyalophora
1231	124.5	8.1	769	2	Q5TN75_ANOGA	Q5tn75	anopheles g
1232	124.5	8.1	819	1	FGFR1_CHICK	P21804	gallus gall
1233	124.5	8.1	848	1	P15083_RAT	P15083	rattus norv
1234	124.5	8.1	886	1	Q9VM64_DROME	Q9vm64	drosophila
1235	124.5	8.1	917	1	ICAM5_MOUSE	O60625	mus musculu
1236	124.5	8.1	954	1	Q7PV74_ANOGA	Q7pv74	anopheles g
1237	124.5	8.1	1007	2	ROBO4_HUMAN	Q8wz75	homo sapien
1238	124.5	8.1	1075	1	Q8TPZ2_METAC	Q8tpz2	methanosarc
1239	124.5	8.1	2217	2	Q8AV57_CHICK	Q8av57	gallus gall
1240	124.5	8.1	4203	2	Q96SG2_CAEEL	Q96sg2	caenorhabdi
1241	124.5	8.1	4219	2	Q9NL87_CAEEL	Q9nl87	caenorhabdi
1242	124.5	8.1	4250	1	Q5PY59_CAEEL	Q5py59	caenorhabdi
1243	124.5	8.1	4369	2	Q5PY59_CAEEL	Q5py59	caenorhabdi
1244	124.5	8.1	4447	2	Q8MXD7_CAEEL	Q8mxd7	caenorhabdi
1245	124.5	8.1	4889	2	Q8MXD8_CAEEL	Q8mxd8	caenorhabdi
1246	124	8.1	243	2	Q9TXK2_CAEEL	Q9txk2	caenorhabdi
1247	124	8.1	316	2	Q9TXK2_CAEEL	Q9txk2	caenorhabdi
1248	124	8.1	336	1	Q61AZ2_HUMAN	Q61az2	homo sapien
1249	124	8.1	380	1	Q5SNN7_BRARE	Q5snn7	brachydanio
1250	124	8.1	388	1	Q46551_9PRIM	Q46551	hylobates s
1251	124	8.1	391	2	Q5T2D2_HUMAN	Q5t2d2	homo sapien
1252	124	8.1	452	1	BASI_RAT	P26453	rattus norv
1253	124	8.1	457	2	Q4S871_RAT	Q4s871	rattus norv
1254	124	8.1	468	2	Q5XKY3_BRARE	Q5xky3	brachydanio
1255	124	8.1	504	2	Q960D1_DROME	Q960d1	drosophila
1256	124	8.1	577	2	Q9XY08_BOMMO	Q9xy08	bombyx mori
1257	124	8.1	584	2	Q98923_CHICK	Q98923	gallus gall
1258	124	8.1	626	2	Q98923_CHICK	Q98923	gallus gall
1259	124	8.1	696	1	Q9D2Z1_MOUSE	Q9d2z1	mus muscu
1260	124	8.1	949	2	Q98921_CHICK	Q98921	gallus gall
1261	124	8.0	1389	2	Q98922_CHICK	Q98922	gallus gall
1262	124	8.0	1400	2	IRPL1_FONPY	Q7yq19	pongo pygma
1263	124	8.0	1958	2	Q8IGN3_DROME	Q8ign3	drosophila
1264	124	8.0	182	2	Q4VA61_MOUSE	Q4va61	mus musculu
1265	123.5	8.0	258	2	Q7PF94_ANOGA	Q7pf94	anopheles g
1266	123.5	8.0	262	2	Q4SE42_TETNG	Q4se42	tetraodon n
1267	123.5	8.0	312	2	Q15232_HUMAN	Q15232	homo sapien
1268	123.5	8.0	379	1	Q5VZT8_HUMAN	Q5vzt8	homo sapien
1269	123.5	8.0	388	1	Q8NAI9_HUMAN	Q8nai9	homo sapien
1270	123.5	8.0	413	2	O66KV0_XENLA	O66kv0	xenopus lae
1271	123.5	8.0	503	1	O8OUI9_MOUSE	O8oui9	mus musculu
1272	123.5	8.0		1	SHPS1_HYACE	P78324	h tyrosine-

#					Name	ID	Organism
1273	123.5	8.0	555	1	CD166_CARAU	Q90304	carassius a
1274	123.5	8.0	662	2	Q8MJZ6_PANTR	Q8mjz6	pan troglod
1275	123.5	8.0	669	2	Q6B515_POEGU	Q6b515	poephila gu
1276	123.5	8.0	796	2	Q91287_PLEWA	Q91287	pleurodeles
1277	123.5	8.0	885	2	Q8N237_HUMAN	Q8n237	homo sapien
1278	123.5	8.0	1000	2	Q4TBR4_TETNG	Q4tbr4	tetraodon n
1279	123.5	8.0	1209	2	P70232_MOUSE	P70232	mus musculu
1280	123	8.0	231	2	Q8WYY6_HUMAN	Q8wyy6	homo sapien
1281	123	8.0	249	1	BASI_CRIGR	Q99pa3	cricetulus
1282	123	8.0	307	2	Q94431_CIOIN	Q94431	ciona intes
1283	123	8.0	351	2	Q6WEB2_BRALA	Q6web2	branchiosto
1284	123	8.0	380	2	Q9H8E9_HUMAN	Q9h8e9	homo sapien
1285	123	8.0	381	2	Q9Y4A4_HUMAN	Q9y4a4	homo sapien
1286	123	8.0	530	2	Q4RTW9_TETNG	Q4rtw9	tetraodon n
1287	123	8.0	812	1	FGFR1_XENLA	P22182	xenopus lae
1288	123	8.0	812	2	Q8N6I2_HUMAN	Q8n6i2	homo sapien
1289	123	8.0	924	2	Q8TAM9_HUMAN	Q8tam9	homo sapien
1290	123	8.0	939	2	Q967X6_DROME	Q967x6	drosophila
1291	123	8.0	949	2	Q9VWZ7_DROME	Q9vwz7	drosophila
1292	123	8.0	242	2	O46604_PIG	O46604	sus scrofa
1293	122.5	7.9	294	2	Q8K125_MOUSE	Q8k125	mus musculu
1294	122.5	7.9	299	1	C80_RABIT	P42070	oryctolagus
1295	122.5	7.9	306	2	Q6GMV6_HUMAN	Q6gmv6	homo sapien
1296	122.5	7.9	314	2	Q5RDG1_PONPY	Q5rdg1	pongo pygma
1297	122.5	7.9	328	2	Q5R884_PONPY	Q5r884	pongo pygma
1298	122.5	7.9	335	1	PSG2_HUMAN	P11465	homo sapien
1299	122.5	7.9	339	2	Q5VTP1_BRARE	Q5vtp1	brachydanio
1300	122.5	7.9	391	2	Q7T1J4_BRARE	Q7t1j4	brachydanio
1301	122.5	7.9	424	2	Q8C6W0_MOUSE	Q8c6w0	mus musculu
1302	122.5	7.9	455	2	Q4RDF3_TETNG	Q4rdf3	tetraodon n
1303	122.5	7.9	606	2	Q9ESS8_RAT	Q9ess8	rattus norv
1304	122.5	7.9	646	1	MUC18_HUMAN	P43121	homo sapien
1305	122.5	7.9	646	2	Q6PHR3_HUMAN	Q6phr3	homo sapien
1306	122.5	7.9	646	2	Q95812_HUMAN	Q95812	homo sapien
1307	122.5	7.9	732	2	Q8CAW4_MOUSE	Q8caw4	mus musculu
1308	122.5	7.9	1001	2	Q5TR64_ANOGA	Q5tr64	anopheles g
1309	122.5	7.9	1505	2	Q7Q623_ANOGA	Q7q623	anopheles g
1310	122.5	7.9	4824	2	Q95YM1_PROCL	Q95ym1	procambarus
1311	122.5	7.9	8625	2	Q86GD6_PROCL	Q86gd6	procambarus
1312	122	7.9	171	2	Q6VZI0_CNPV	Q6vzi0	canarypox v
1313	122	7.9	243	1	CD48_HUMAN	P09326	homo sapien
1314	122	7.9	243	2	Q5U055_HUMAN	Q5u055	homo sapien
1315	122	7.9	272	2	Q6GT74_RAT	Q6gt74	rattus norv
1316	122	7.9	279	2	Q9UD50_HUMAN	Q9ud50	homo sapien
1317	122	7.9	325	2	Q7Z6M3_HUMAN	Q7z6m3	homo sapien
1318	122	7.9	402	1	IRPL2_HUMAN		homo sapien
1319	122	7.9	402	1	RAGE_RAT	Q63495	rattus norv
1320	122	7.9	459	2	Q9JHL6_RAT	Q9jhl6	rattus norv
1321	122	7.9	477	2	Q5EAJ2_FUGRU	Q5eaj2	fugu rubrip
1322	122	7.9	537	2	Q7QEY8_ANOGA	Q7qey8	anopheles g
1323	122	7.9	557	2	Q4T6S0_TETNG	Q4t6s0	tetraodon n
1324	122	7.9	571	2	Q5EG07_ICTPU	Q5eg07	ictalurus p
1325	122	7.9	605	2	Q8TBU0_HUMAN	Q8tbu0	homo sapien
1326	122	7.9	686	1	IRPL2_MOUSE	Q9ere6	mus musculu
1327	122	7.9	693	2	Q9UPU1_HUMAN	Q9upu1	homo sapien
1328	122	7.9	696	2	Q9NZN1_HUMAN	Q9nzn1	homo sapien
1329	122	7.9	696	1	IRPL1_PANTR	P60029	pan troglod
1330	122	7.9	696	1	IRPL1_HUMAN	Q5jyv0	homo sapien
1331	122	7.9	771	1	PIGR_MOUSE	O70570	mus musculu
1332	122	7.9	881	2	O60UL6_CAEBR	O60ul6	caenorhabdi
1333	122	7.9	1150	2	Q8BS24_MOUSE	Q8bs24	mus musculu
1334	122	7.9	1375	2	Q8ML47_DROME	Q8ml47	drosophila
1335	122	7.9	1375	2	Q94537_DROME	Q94537	drosophila
1336	122	7.9	1526	2	Q94538_DROME	Q94538	drosophila
1337	122	7.9	1526	2	Q9V6D5_DROME	Q9v6d5	drosophila
1338	121.5	7.9	189	2	Q15230_HUMAN	Q15230	homo sapien
1339	121.5	7.9	199	2	Q8NDI0_HUMAN	Q8ndi0	homo sapien
1340	121.5	7.9	230	2	Q8QGS1_COTJA	Q8qgs1	coturnix co
1341	121.5	7.9	233	2	Q6NS96_HUMAN	Q6ns96	homo sapien
1342	121.5	7.9	258	2	Q12811_HUMAN	Q12811	homo sapien
1343	121.5	7.9	298	2	Q8INK5_DROME	Q8ink5	drosophila
1344	121.5	7.9	318	2	Q8BEI6_VARV	Q8bei6	variola vir
1345	121.5	7.9	318	2	Q9QNG4_VARV	Q9qng4	variola min
1346	121.5	7.9	336	2	Q961T8_DROME	Q961t8	drosophila
1347	121.5	7.9	357	2	Q63238_RAT	Q63238	rattus norv
1348	121.5	7.9	404	1	RAGE_HUMAN	Q15109	homo sapien
1349	121.5	7.9	635	2	Q4SIS8_TETNG	Q4sis8	tetraodon n
1350	121.5	7.9	700	1	KIRR2_MOUSE	Q7tsu7	mus musculu
1351	121.5	7.9	700	2	O18433_GEOCY	O18433	geodia cydo
1352	121.5	7.9	733	2	Q92QM7_MOUSE	Q92qm7	mus musculu
1353	121.5	7.9	782	2	Q9TTZ3_RABIT	Q9ttz3	oryctolagus
1354	121.5	7.9	782	2	Q61563_MOUSE	Q61563	mus musculu
1355	121.5	7.9	893	2	Q5TNT4_ANOGA	Q5tnt4	anopheles g
1356	121.5	7.9	1177	2	Q6GQB1_XENLA	Q6gqb1	xenopus lae
1357	121.5	7.9	1447	1	DCC_MOUSE	P70211	mus musculu
1358	121.5	7.9	1471	2	O18245_CAEEL	O18245	caenorhabdi
1359	121.5	7.9	265	2	Q61XU3_CAEBR	Q61xu3	caenorhabdi
1360	121	7.8	275	1	VOSS_FOWPV	P21975	fowlpox vir
1361	121	7.8	275	2	Q70H96_FOWPV	Q70h96	fowlpox vir
1362	121	7.8	336	2	Q8UV73_BRARE	Q8uv73	brachydanio
1363	121	7.8	402	2	O35444_MOUSE	O35444	mus musculu
1364	121	7.8	446	2	Q63236_RAT	Q63236	rattus norv
1365	121	7.8	475	2	Q4V8L5_RAT	Q4v8l5	rattus norv
1366	121	7.8	695	1	IRPL1_MOUSE	P59823	mus musculu
1367	121	7.8	696	1	IRPL1_RAT	P59824	rattus norv
1368	121	7.8	775	2	Q6FF50_XENLA	Q6ff50	xenopus lae
1369	121	7.8	822	2	Q9QVV7_9MURI	Q9qvv7	rattus sp.
1370	121	7.8	844	2	Q5XG38_XENLA	Q5xg38	xenopus lae
1371	121	7.8	847	1	FSTL5_MOUSE	Q8bfr2	mus musculu
1372	121	7.8	858	2	Q5TYT7_BRARE	Q5tyt7	brachydanio
1373	121	7.8	1437	2	O44329_HIRME	O44329	hirudo medi
1374	121	7.8	2007	2	Q4SM88_TETNG	Q4sm88	tetraodon n
1375	121	7.8	3158	2	Q4TAD4_TETNG	Q4tad4	tetraodon n
1376	120.5	7.8	181	2	Q9D7V7_MERUN	Q9d7v7	meriones un
1377	120.5	7.8	217	2	Q6KGN0_9CAUD	Q6kgn0	bacteriopha
1378	120.5	7.8	227	2	Q6KGN1_9CAUD	Q6kgn1	bacteriopha
1379	120.5	7.8	229	2	Q568D3_BRARE	Q568d3	brachydanio
1380	120.5	7.8	265	2	Q4V3R1_DROME	Q4v3r1	drosophila
1381	120.5	7.8	292	2	Q80W97_MERUN	Q80w97	meriones un
1382	120.5	7.8	294	2	Q9VMB2_DROME	Q9vmb2	drosophila
1383	120.5	7.8	315	2	Q684Q2_MOUSE	Q684q2	mus musculu
1384	120.5	7.8	332	2	Q8UUG6_BRARE	Q8uug6	brachydanio
1385	120.5	7.8	335	2	Q4V3F0_DROME	Q4v3f0	drosophila
1386	120.5	7.8	376	2	Q7SX76_BRARE	Q7sx76	brachydanio
1387	120.5	7.8	483	2	Q5W0G0_HUMAN	Q5w0g0	homo sapien
1388	120.5	7.8	571	2	Q8QHL2_CHICK	Q8qhl2	gallus gall
1389	120.5	7.8	677	2	Q6GNS5_XENLA	Q6gns5	xenopus lae
1390	120.5	7.8	827	2	Q8N7W7_HUMAN	Q8n7w7	homo sapien
1391	120	7.8	1122	2	Q5U4L8_XENLA	Q5u4l8	xenopus lae
1392	120	7.8	4194	2	Q9VB35_DROME	Q9vb35	drosophila
1393	120	7.8	248	2	Q5RID5_BRARE	Q5rid5	brachydanio
1394	120	7.8	249	2	Q8JFR5_BRARE	Q8jfr5	brachydanio
1395	120	7.8	296	2	Q9W755_DROME	Q9w755	drosophila
1396	120	7.8	308	2	Q7KUK9_DROME	Q7kuk9	drosophila
1397	120	7.8	337	2	Q55108_MOUSE	Q55108	mus musculu
1398	120	7.8	355	2	Q6XJV4_MOUSE	Q6xjv4	mus musculu
1399	120	7.8	600	2	Q6XJV6_MOUSE	Q6xjv6	mus musculu
1400	120	7.8	795	2	Q6LCE6_HUMAN	Q6lce6	homo sapien
1401	120	7.8	939	2	Q7Q863_ANOGA	Q7q863	anopheles g
1402	120	7.8	976	2	Q9IA24_9PERC	Q9ia24	sphaeroides
1403	120	7.8	976	2	Q4V8L4_RAT	Q4v8l4	rattus norv
1404	120	7.8	976	2	Q8V8L4_RAT	Q8v8l4	rattus norv
1405	120	7.8	1501	2	Q7KUK9_DROME	Q7kuk9	drosophila
1406	119.5	7.8	257	2	Q8AY28_VARV	Q8ay28	variola vir
1407	119.5	7.8	270	2	Q5EG08_ICTPU	Q5eg08	ictalurus p
1408	119.5	7.8	318	2	O08266_ICTPU	O08266	ictalurus p
1409	119.5	7.8	343	2	Q15403_HUMAN	Q15403	homo sapien
1410	119.5	7.8	352	2	Q5WRR1_CAEEL	Q5wrr1	caenorhabdi
1411	119.5	7.7	352	2	Q4RGD6_CAEEL	Q4rgd6	caenorhabdi
1412	119.5	7.7	452	2	Q53TU7_HUMAN	Q53tu7	homo sapien
1413	119.5	7.7	452	2	Q52KG8_MOUSE	Q52kg8	mus musculu
1414	119.5	7.7	464	1	KIT_CHICK		gallus gall
1415	119.5	7.7	556	2	Q7QJK6_ANOGA	Q7qjk6	anopheles g
1416	119.5	7.7	834	2	Q8I156_GALLUS	Q8i156	gallus gall
1417	119.5	7.7	960	1	Q5RKM8_MOUSE	Q5rkm8	mus musculu
1418	119.5	7.7	1100	2	Q5RKM8_MOUSE	Q5rkm8	mus musculu

1419	119.5	7.7	10578	2	Q8ISF5_CAEEL	caenorhabdi
1420	119	7.7	413	2	Q69P0_ANTPE	antheraea p
1421	119	7.7	422	2	Q86CY9_HELAM	helicoverpa
1422	119	7.7	577	2	Q80Y42_MOUSE	mus musculu
1423	119	7.7	620	2	Q48IC0_TETNG	tetraodon n
1424	119	7.7	675	2	Q4SSQ4_TETNG	tetraodon n
1425	119	7.7	880	2	Q7KPQ8_DROME	drosophila
1426	119	7.7	1187	2	Q589G5_CHICK	gallus gall
1427	119	7.7	1390	2	Q9VN14_DROME	drosophila
1428	119	7.7	1390	2	Q5BI91_DROME	drosophila
1429	118.5	7.7	163	2	Q8K1H8_MOUSE	mus musculu
1430	118.5	7.7	269	2	Q5RC22_PONPY	pongo pygma
1431	118.5	7.7	285	2	Q5SNN8_BRARE	brachydanio
1432	118.5	7.7	302	2	Q5YJ10_SHEEP	ovis aries
1433	118.5	7.7	342	2	P97635_RAT	rattus norv
1434	118.5	7.7	352	2	O76697_CAEEL	caenorhabdi
1435	118.5	7.7	379	2	SIGL7_HUMAN	homo sapien
1436	118.5	7.7	397	2	Q8BLX5_MOUSE	mus musculu
1437	118.5	7.7	467	1	SIGL7_HUMAN	homo sapien
1438	118.5	7.7	528	2	P91670_DROME	drosophila
1439	118.5	7.7	538	2	Q9NWQ7_HUMAN	homo sapien
1440	118.5	7.7	540	2	Q8N029_HUMAN	homo sapien
1441	118.5	7.7	545	2	Q9VCT4_DROME	drosophila
1442	118.5	7.7	582	2	Q95N25_BOVIN	bos taurus
1443	118.5	7.7	606	2	Q6IRH8_RAT	rattus norv
1444	118.5	7.7	697	1	SIG10_HUMAN	homo sapien
1445	118.5	7.7	717	2	Q7PUQ1_ANOGA	anopheles g
1446	118.5	7.7	912	2	ICAM5_RABIT	oryctolagus
1447	118.5	7.7	1187	2	Q8WR45_CAEEL	caenorhabdi
1448	118.5	7.7	1195	2	Q5TUS2_ANOGA	anopheles g
1449	118.5	7.7	1228	2	Q7QEI6_ANOGA	anopheles g
1450	118.5	7.7	1464	2	Q4SKS5_TETNG	tetraodon n
1451	118.5	7.7	2646	2	Q4SLN8_TETNG	tetraodon n
1452	118	7.6	175	2	Q4TGY2_TETNG	tetraodon n
1453	118	7.6	226	2	Q7PUJ2_ANOGA	anopheles g
1454	118	7.6	233	2	Q6PIW7_HUMAN	homo sapien
1455	118	7.6	253	2	O17858_CAEEL	caenorhabdi
1456	118	7.6	270	2	Q8BTN8_MOUSE	mus musculu
1457	118	7.6	290	2	Q5TNT8_ANOGA	anopheles g
1458	118	7.6	321	2	Q8IWY0_HUMAN	homo sapien
1459	118	7.6	351	2	Q7QOP8_ANOGA	anopheles g
1460	118	7.6	381	2	Q4SDA6_TETNG	tetraodon n
1461	118	7.6	385	2	Q4SQV8_TETNG	tetraodon n
1462	118	7.6	421	2	Q9NT99_HUMAN	homo sapien
1463	118	7.6	430	2	Q58F20_HUMAN	homo sapien
1464	118	7.6	553	2	Q8WXJ5_HUMAN	homo sapien
1465	118	7.6	620	1	SMP_COTJA	coturnix co
1466	118	7.6	626	2	Q90880_CHICK	gallus gall
1467	118	7.6	692	2	Q4RV46_TETNG	tetraodon n
1468	118	7.6	722	2	Q6GNB3_XENLA	xenopus lae
1469	118	7.6	769	2	Q8NI15_HUMAN	homo sapien
1470	118	7.6	806	2	CEK2_CHICK	gallus gall
1471	118	7.6	806	1	FGFR3_HUMAN	homo sapien
1472	118	7.6	814	2	Q91897_XENLA	xenopus lae
1473	118	7.6	838	2	Q8WXJ7_HUMAN	homo sapien
1474	118	7.6	847	1	FSTL5_HUMAN	homo sapien
1475	118	7.6	879	2	Q5FL9_HUMAN	homo sapien
1476	118	7.6	924	1	ICAM5_HUMAN	homo sapien
1477	118	7.6	1203	2	Q4SRR2_TETNG	tetraodon n
1478	118	7.6	1415	2	Q94155_CAEEL	caenorhabdi
1479	117.5	7.6	163	2	Q9NVJ5_HUMAN	homo sapien
1480	117.5	7.6	391	2	Q59EJ9_HUMAN	homo sapien
1481	117.5	7.6	398	2	Q9Y640_HUMAN	homo sapien
1482	117.5	7.6	403	2	RAGE_MOUSE	mus musculu
1483	117.5	7.6	467	2	Q91VT9_MOUSE	mus musculu
1484	117.5	7.6	467	2	Q8C6F2_MOUSE	mus musculu
1485	117.5	7.6	538	1	PVR2_HUMAN	homo sapien
1486	117.5	7.6	556	1	ILRL1_HUMAN	homo sapien
1487	117.5	7.6	597	1	SIG11_PANTR	pan troglod
1488	117.5	7.6	603	2	Q9NKF5_DROME	drosophila
1489	117.5	7.6	743	2	Q6P4H5_HUMAN	homo sapien
1490	117.5	7.6	764	1	PIGR_HUMAN	homo sapien
1491	117.5	7.6	764	2	Q8IZY7_HUMAN	homo sapien
1492	117.5	7.6	764	2	Q68D81_HUMAN	homo sapien
1493	117.5	7.6	793	2	Q4RY64_TETNG	tetraodon n
1494	117.5	7.6	848	2	Q25198_HYDAT	hydra atten
1495	117.5	7.6	1089	1	PGFRA_HUMAN	homo sapien
1496	117.5	7.6	1198	2	Q60T65_CAEBR	caenorhabdi
1497	117.5	7.6	1240	1	NFASC_MOUSE	mus musculu
1498	117.5	7.6	1251	2	Q62Q54_MOUSE	mus musculu
1499	117.5	7.6	2343	2	Q5TX11_ANOGA	anopheles g
1500	117.5	7.6	6710	2	Q61SF4_CAEBR	caenorhabdi

ALIGNMENTS

RESULT 1
JAM1_HUMAN

```
ID   JAM1_HUMAN     STANDARD;      PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE   molecule 1) (JAM) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11
DE   receptor).
GN   Name=F11R; Synonyms=JAM1, JCAM, ORFNames=UNQ264/PRO301;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=10753840;
RA   Sobocka M.B., Sobocki T., Banerjee P., Weiss C., Rushbrook J.I.,
RA   Norin A.J., Hartwig J., Salifu M.O., Markell M.S., Babinska A.,
RA   Ehrlich Y.H., Kornecki E.;
RT   "Cloning of the human platelet F11 receptor: a cell adhesion molecule
RT   member of the immunoglobulin superfamily involved in platelet
RT   aggregation.";
RL   Blood 95:2600-2609(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND SUBCELLULAR LOCATION.
RP   PubMed=11171323;
RA   Naik U.P., Naik M.U., Eckfeld K., Martin-DeLeon P., Spychala J.;
RT   "Characterization and chromosomal localization of JAM-1, a platelet
RT   receptor for a stimulatory monoclonal antibody.";
RL   J. Cell Sci. 114:539-547(2001).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
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RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yanuar Y.J., Yi S., Yu C., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA   Blakesley R.W., Touchman J.W.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   PROTEIN SEQUENCE OF 28-103 AND 123-130, AND N-GLYCOSYLATION.
RA   Naik U.P., Ehrlich Y.H., Kornecki E.;
RX   PubMed=7646439;
RT   "Mechanisms of platelet activation by a stimulatory antibody: cross-
RT   linking of a novel platelet receptor for monoclonal antibody F11 with
RT   the Fc gamma RII receptor.";
RL   Biochem. J. 310:155-162(1995).
RN   [8]
RP   PROTEIN SEQUENCE OF 28-42.
RC   TISSUE=Platelet;
RX   MEDLINE=2608298; PubMed=12665801; DOI=10.1038/nbt810;
RA   Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA   Thomas G.R., Vandekerckhove J.;
RT   "Exploring proteomes and analyzing protein processing by mass
RT   spectrometric identification of sorted N-terminal peptides.";
RL   Nat. Biotechnol. 21:566-569(2003).
RN   [9]
RP   PROTEIN SEQUENCE OF 28-39.
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [10]
RP   INTERACTION WITH MPDZ.
RX   MEDLINE=21489913; PubMed=11483047;
RA   Itoh M., Sasaki H., Furuse M., Ozaki H., Kita T., Tsukita S.;
RT   "Junctional adhesion molecule (JAM) binds to PAR-3: a possible
RT   mechanism for the recruitment of PAR-3 to tight junctions.";
RL   J. Cell Biol. 154:491-497(2001).
RN   [11]
RP   REVIEW, AND NOMENCLATURE.
RX   PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA   Muller W.A.;
RT   "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT   and the inflammatory response.";
RL   Trends Immunol. 24:327-334(2003).

CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC   formation. Appears early in primordial forms of cell junctions and
CC   recruits PARD3. The association of the PARD6-PARD3 complex may
CC   prevent the interaction of PARD3 with JAM1, thereby preventing
CC   tight junction assembly (By similarity). Plays a role in
CC   regulating monocyte transmigration involved in integrity of
CC   epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC   association between PARD3 and PARD6B probably disrupts this
CC   interaction (By similarity). Interacts with the ninth PDZ domain
CC   of MPDZ.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   Localized at tight junctions of both epithelial and endothelial
CC   cells.
CC   -!- PTM: N-Glycosylated.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC   domains.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF111713; AAD42050.1; -; mRNA.
DR   EMBL; AF207907; AAF22829.1; -; mRNA.
DR   EMBL; AF172398; AAD48877.1; -; mRNA.
DR   EMBL; AL136549; CAB66584.1; -; mRNA.
DR   EMBL; AY358896; AAQ89255.1; -; mRNA.
DR   EMBL; BC001533; AAH01533.1; -; mRNA.
DR   PIR; A59406; S56749.
DR   PDB; 1NBO; X-ray; A/B=27-233.
DR   HGNC; HGNC:14685; F11R.
DR   Ensembl; ENSG00000158769; Homo sapiens.
DR   MIM; 605721; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
FT   SIGNAL   1   27
FT   CHAIN   28   299   Junctional adhesion molecule A.
FT   TOPO_DOM   28   238   Extracellular (Potential).
FT   TRANSMEM   239   259   Potential.
FT   TOPO_DOM   260   299   Cytoplasmic (Potential).
FT   DOMAIN   28   125   Ig-like V-type 1.
FT   DOMAIN   135   228   Ig-like V-type 2.
FT   CARBOHYD   185   185   N-linked (GlcNAc...) (Potential).
FT   DISULFID   50   109   Potential.
FT   DISULFID   153   212   Potential.
SQ   SEQUENCE   299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match   100.0%; Score 1544; DB 1; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.8e-111;
Matches   299; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYYTCMVSEBGGNSYG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYYTCMVSEBGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPEYTWFKDGIVMPTNPKST 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

RESULT 2

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

ID   Q6F1B4_HUMAN
AC   Q6F1B4;
ID   Q6F1B4_HUMAN PRELIMINARY;   PRT;   299 AA.
AC   Q6F1B4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   F11R protein (F11 receptor protein) (JAM1) (Hypothetical protein
DE   FLJ90671).
GN   Name=F11R; ORFNames=RP11-544M22.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20537956; PubMed=11087121; DOI=10.1080/15216540050176593;
RA   Gupta S.K., Pillarisetti K., Ohlstein E.H.;
RT   "Platelet agonist F11 receptor is a member of the immunoglobulin
RT   superfamily and identical with junctional adhesion molecule (JAM):
RT   regulation of expression in human endothelial cells and macrophages.";
RL   IUBMB Life 50:51-56(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22701983; PubMed=12817473; DOI=10.1515/BC.2003.085;
RA   Wenzel K., Felix S.B., Flachmeier C., Heere P., Schulze W.,
RA   Grunewald I., Pankow H., Hewelt A., Scherneck S., Bauer D.;
RT   Hoehe M.R.;
RT   "Identification and characterization of KAT, a novel gene
RT   preferentially expressed in several human cancer cell lines.";
RL   Biol. Chem. 384:763-775(2003).
RN   [4]
DR   Ensembl; ENSG00000158769; Homo sapiens.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%; Pred. No. 1.8e-111;
Matches 299; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNNGVIV 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNNGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 3

ID   Q9Y5B2_HUMAN
AC   Q9Y5B2;
ID   Q9Y5B2_HUMAN PRELIMINARY;   PRT;   259 AA.
AC   Q9Y5B2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA   Foley C., Parkos C.A.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR   EMBL; AF154005; AAD43794.1; -; mRNA.
DR   HSSP; Q9Y224; 1NBQ.
SMR   Q9Y5B2; 20-193.
DR   Ensembl; ENSG00000158769; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; Ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane.
SQ   SEQUENCE   259 AA; 28122 MW; FE38521A91158280 CRC64;

Query Match   83.0%; Score 1281; DB 2; Length 259;
Best Local Similarity   86.0%; Pred. No. 3.8e-91;
Matches 257; Conservative   0; Mismatches   2; Indels   40; Gaps   2;

```
Qy     1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MGTKAQVERKLLCLFILAIL-----------------------PENNPVKLSCAYSGFSSPR- 39

Db     1 -----------------------------AASYEDRVTFLPTGITFKSVTREDTGTYTCMVFEBGGNSYG 80

Qy    61 EWKFDQGDTTRLVCVNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEBGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
Db    81 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 140

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
Db   141 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 200

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
Db   201 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 259
```

RESULT 4
ID   JAM1_BOVIN   STANDARD;   PRT;   298 AA.
AC   Q9XT56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE   molecule 1) (JAM).
GN   Name=F11R; Synonyms=JAM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99329940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC   formation. Appears early in primordial forms of cell junctions and
CC   recruits PARD3. The association of the PARD6-PARD3 complex may
CC   prevent the interaction of PARD3 with JAM1, thereby preventing
CC   tight junction assembly (By similarity). Plays a role in
CC   regulating monocyte transmigration involved in integrity of
CC   epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC   association between PARD3 and PARD6B probably disrupts this
CC   interaction. Interacts with the ninth PDZ domain of MPDZ (By
CC   similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   Localized at tight junctions of both epithelial and endothelial
CC   cells (By similarity).
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC   domains.
CC   --
DR   EMBL; AF111714; AAD42051.1; -; mRNA.
DR   HSSP; Q9Y624; 1NBQ.
DR   SMR; Q9XT56; 24-232.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG LIKE; 2.
KW   Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction;
KW   Transmembrane.
FT   SIGNAL   1   24   Potential.
FT   CHAIN   25   298   Junctional adhesion molecule A.
FT   TOPO_DOM   25   237   Extracellular (Potential).
FT   TRANSMEM   238   258   Potential.
FT   TOPO_DOM   259   298   Cytoplasmic (Potential).
FT   DOMAIN   28   124   Ig-like V-type 1.
FT   DOMAIN   134   227   Ig-like V-type 2.
FT   CARBOHYD   184   184   N-linked (GlcNAc...) (Potential).
FT   DISULFID   49   108   Potential.
FT   DISULFID   152   211   Potential.
SQ   SEQUENCE   298 AA; 32456 MW; 714FB1C171476D9A2 CRC64;

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Qy     1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
           ||||||||||||||||||||||| :|||||||||||||||||||||||||||||||||||
Db     1 MGTKARVGSTELLIF-TSMILCSLALGRGAVQTYEPVVRVPENNPAKLSCSYSGFSSPRV 59

Qy    61 EWKFDQGDTTRLVCVNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEBGGNSYG 120
           ||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    60 EWKFTHGDIRGLVCVNNKITASYENRVTFSDTGITFHSVTRKDTGMYTCMVSDEGGNTYG 119

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
           ||||| |||||||||||| |||| ||||||||||||||||||||||  ||||| ||||
Db   120 EVTVQLIVLVPPSKPIINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEPKSN 179

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
           ||||||| ||:||||| |||| |||||||:|| | || |  |   |      | ||||
Db   180 RAFSNSSYTLNQKTGELIFDPVSASDTGDFTCQAQGYASPVKSDTVHMDAVELNVGGIV 239

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
           || | |||||| ||||||||||||:|||  || :||||||||||||| |||: ||||||
Db   240 AAVFVTLILLGALIFGIWFAYSRGYFDRAKKGTSNKKVIYSQPNARSDGEFRQTSSFLV 298
```

Query Match   76.2%; Score 1176.5; DB 1; Length 298;
Best Local Similarity   74.6%; Pred. No. 5.6e-83;
Matches 223; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

RESULT 5
ID   Q5E9V8_BOVIN   Q5E9V8_BOVIN PRELIMINARY;   PRT;   298 AA.
AC   Q5E9V8;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   F11 receptor isoform a.
GN   Name=F11R;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pooled;
RX   MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA   Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA   Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA   Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA   Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA   Keele J.W.;
RT   "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT   libraries and construction of a gene index for cattle.";
RL   Genome Res. 11:626-630(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pooled;
RA   Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,

(Left column)

RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT020812; AAX08829.1; -; mRNA.
KW Receptor.
SQ SEQUENCE 298 AA; 32456 MW; 714FE1C171476S9A2 CRC64;

Query Match 76.2%; Score 1176.5; DB 2; Length 298;
Best Local Similarity 74.6%; Pred. No.5.6e-83;
Matches 223; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

```
Qy    1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60
          |:|||:|||||||||||||:||:::|||||||||||||  |::||||||||||:|||||||
Db    1 MGTKARVGSTELLF-TSMILCSLALGRGAVQTYEPVVRVPENNPAKLSCSYSGFSSPRV   59

Qy   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
          ||||  |:|||:||||||||||||||:|||||||||:|||||:|||:|||||||::|||
Db   60 EWKFTHGDIRGLVCYNNKITASYENRVTFSDTGITFHSVTRKDTGMYTCMVSDEGGNTYG  119

Qy  121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180
          ||.|:||||||||||:|||||.:|||:|||||||||:||||||||:||||||::||||:||
Db  120 EVTVQLIVLVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEPKSN  179

Qy  181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240
          |||||||.|||:.|||:||||.||||||:.:|.|.||||.|:.:..|||.||||.||..||
Db  180 RAFSNSSYTLNQKTGELIFDPVSASDTGDFTCQAQNGYASPVKSDTVHMDAVELNVGGIV  239

Qy  241 AAVLVTLILLGILLVFGIWFAYSRGRHPDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
          |||.||||||.|.|.|||||||||||  :|:|||||:|||||||||.||:|||:||||||||
Db  240 AAVFVTLILLGALIFGIWFAYSRGYFDRAKKGTSNKKVIYSQPNARSDGEFRQTSSFLV   298
```

RESULT 6

ID JAM1_RAT STANDARD; PRT; 300 AA.
AC Q9JHY1;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE molecule 1) (JAM).
GN Name=F11r; Synonyms=Jam1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RA Mashima H., Kojima I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Seems to play a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PARD3. The association of PARD3 with JAM1, thereby preventing
CC prevent the interaction of the PARD6-PARD3 complex may
CC tight junction assembly. Plays a role in regulating monocyte
CC transmigration involved in integrity of epithelial barrier.
CC Involved in platelet activation (By similarity).
CC -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC association between PARD3 and PARD6B probably disrupts this
CC interaction. Interacts with the ninth PDZ domain of MPDZ (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
CC cells (By similarity).
CC -!- PTM: N-Glycosylated (By similarity).

(Right column)

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC domains.

DR EMBL; AF276998; AAF78250.1; -; mRNA.
DR EMBL; BC065309; AAH65309.1; -; mRNA.
DR HSSP; Q9JHY1; 1F97.
DR SMR; Q9JHY1; 27-238.
DR Ensembl; ENSRNOG00000004414; Rattus norvegicus.
DR RGD; 621842; F11r.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction;
KW Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 300 Junctional adhesion molecule A.
FT TOPO_DOM 27 238 Extracellular (Potential).
FT TRANSMEM 239 259 Potential.
FT TOPO_DOM 260 300 Cytoplasmic (Potential).
FT DOMAIN 28 122 Ig-like V-type 1.
FT DOMAIN 134 228 Ig-like V-type 2.
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
FT DISULFID 49 108 By similarity.
FT DISULFID 152 212 By similarity.
SQ SEQUENCE 300 AA; 32370 MW; 45AE362A96158BFA CRC64;

Query Match 71.0%; Score 1096.5; DB 1; Length 300;
Best Local Similarity 71.8%; Pred. No.9e-77;
Matches 216; Conservative 33; Mismatches 49; Indels 3; Gaps 3;

```
Qy    1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV    60
          |:|.:.|.|.||:|LF-TSMILGSLVQGKGSVSYSPQTRAVQVPEND.SVKLPCIYSGFSSPRV
Db    1 MGTEGKAGSKLLFLF-TSMILGSLVQGKGSVSYSPQTRAVQVPENDSVKLPCIYSGFSSPRV  59

Qy   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120
          ||||  |.|:|.|||||||:|..|.|||||.....|||.||||.|.|.||||||.:||.||
Db   60 EWKFVQGSTTALVCYNNQITVPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEDGGQNYG  119

Qy  121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPT-NPKS  179
          || . ::| |.VPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEY.WFKDGV.M.TADAKK
Db  120 EVSIHLITVLVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKK  179

Qy  180 TRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI  239
          ||||.|||....|.||:||||.|||.|||||.|..||||||.|.|.|||||||.||..||
Db  180 TRAFINSSYTIDPKSGDLVFDPVSAFDSGEYCEAQNGYGTAMRSEAVRMEAVELNVGGI  239

Qy  240 VAAVLVTLILLGILLVFGIWFAYSRGRHPDRTKKGTS-SKKVIYSQPSARSEGEFKQTSSFL  298
          |||||||||||.|.|:|||||||||||  :|||||::..|||||||||||||||||||||||
Db  240 VAAVLVTLILLGLLIFGIWFAYSRGYFERTKKGTAPGKKVIYSQPSARSEGEFKQTSSFL  299

Qy  299 V  299
          |
Db  300 V  300
```

RESULT 7

ID Q8VC39_MOUSE PRELIMINARY; PRT; 300 AA.
AC Q8VC39;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE F11r protein (Mus musculus adult male cecum cDNA, RIKEN full-length
DE enriched library, clone:9130004G24 product:junction cell adhesion

```
DE   molecule, full insert sequence).
GN   Name=Fllr;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mix FVB/N;
RC   TISSUE=Mammary tumor, WAP-TGF alpha model. 7 months old;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.24603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mix FVB/N;
RC   TISSUE=Mammary tumor, WAP-TGF alpha model. 7 months old;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Muntermann E., Schatten R., Henze S., Bohn E.,
RA   Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT   "Cloning of mouse full open reading frames in Gateway(R) system entry
RT   vector (pDONR201).";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
```

```
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   the RIKEN Genome Exploration Research Group Phase I & II Team;
RP   STRAIN=C57BL/6J; TISSUE=Cecum;
RA   The FANTOM Consortium;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda H., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021876; AAH21876.1; -; mRNA.
DR   EMBL; CT010347; CAJ18555.1; -; mRNA.
DR   EMBL; AK033574; BAC28369.1; -; mRNA.
DR   HSSP; O88792; 1F97.
DR   SMR; Q8VC39; 27-238.
DR   Ensembl; ENSMUSG00000038235; Mus musculus.
DR   MGI; MGI:1321398; Fllr.
DR   GO; GO:0005923; C:tight junction; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007155; P:cell adhesion; IDA.
DR   GO; GO:0030855; P:epithelial cell differentiation; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   300 AA;  32424 MW;  3CB561E8FF3B97EC CRC64;
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Query Match             69.9%;  Score 1079.5;  DB 2;  Length 300;
Best Local Similarity   68.4%;  Pred. No. 1.9e-75;
Matches  206;  Conservative   44;  Mismatches   48;  Indels    3;  Gaps    3;

Qy          1 MGTKAQVERKLLCLFIALLLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
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Qy    1  MGTEGKAGRKLLPLF-TSMILGSLVQGKGSVTAQSDVQVPENESIKILTCTYSGFSSPRV    59
            ||||||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGTEGKAGRKLLFLF-TSMILGSLVQGKGSVTAQSDVQVPENESIKILTCTYSGFSSPRV    59

Qy   61  EWKFPDGQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG   120
            ||||  |  ||  ||||| ||||| | |||||    || |||| |  |||||||||| .||
Db   60  EWKFVQGSTPALVCYNSQITAPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEEGGQNYG   119

Qy  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLITCSEQDGSPPSEYTWFKDGIVMPT-NPKS   179
            || .|| |||||||||| .|.|| |||||||.|||| ||||||||| |||||| .|  .||||
Db  120  EVSIHLTVLVPPSKPTISVPSSSVTIGNRAVLTCSEEHDGSPPSEYEWFKDGISMLTADAKK   179

Qy  180  TRAFSNSSYVLNPTTGELVFDDLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI   239
            ||||  .|| ..|  |.|.|| |  |.||||.|.|.||||| | |.||  ||.|| ||| .|
Db  180  TRAFPMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSERAAHMDAVELNVGGI   239

Qy  240  VAALVLTLILGILIFGVWFAYSRGYFPERTKKGTAPGKKVVIYSQPSTRSEGEFKQTSSFL   299
            |||||||||||  |||||||| ||||||||||||||||||||| ||||||||||||||||||
Db  240  VAALVLTLILGLLIFGVWFAXSRGYFPERTKKGTAPGKKVVISQPSTRSEGEFKQTSSFL    298

Qy  299  V   299
            |
Db  300  |   300
```

RESULT 8
JAM1_MOUSE

ID   JAM1_MOUSE   STANDARD;   PRT;   300 AA.
AC   Q9JII6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion
DE   molecule 1) (JAM).
GN   Name=F11r; Synonyms=Jam1, Jcam, Jcam1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99327120; PubMed=9660867; DOI=10.1083/jcb.142.1.117;
RA   Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA   Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA   Simmons D., Dejana E.;
RT   "Junctional adhesion molecule, a novel member of the immunoglobulin
RT   superfamily that distributes at intercellular junctions and modulates
RT   monocyte transmigration.";
RL   J. Cell Biol. 142:117-127(1998).
RN   [2]
RP   INTERACTION WITH PARD3.
RX   MEDLINE=21340266; PubMed=11481715; DOI=10.1093/emboj/20.16.4391;
RA   Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA   Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
RT   "The cell polarity protein ASIP/PAR-3 directly associates with
RT   junctional adhesion molecule (JAM).";
RL   EMBO J. 20:3738-3748(2001).
RN   [3]
RA   Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an emerging junctional adhesion molecular
RT   family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX   MEDLINE=21391702; PubMed=11500266; DOI=10.1093/emboj/20.14.3738;
RA   Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA   Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA   Winkler F.K., Hennig M.;
RT   "X-ray structure of junctional adhesion molecule: structural basis for
RT   homophilic adhesion via a novel dimerization motif.";
RL   EMBO J. 20:4391-4398(2001).
RN   [5]
RP   REVIEW, AND NOMENCLATURE.
RX   MEDLINE=22695901; PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA   Muller W.A.;
RT   "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT   and the inflammatory response.";
RL   Trends Immunol. 24:327-334(2003).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC   formation. Appears early in primordial forms of cell junctions and
CC   recruits PARD3. The association of the PARD6-PARD3 complex may
CC   prevent the interaction of PARD3 with JAM1, thereby preventing
CC   tight junction assembly. Plays a role in regulating monocyte
CC   transmigration involved in integrity of epithelial barrier.
CC   Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the ninth PDZ domain of MPDZ (By
CC   similarity). Interacts with the first PDZ domain of PARD3. The
CC   association between PARD3 and PARD6B probably disrupts this
CC   interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   Localized at tight junctions of both epithelial and endothelial
CC   cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
CC   domains.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; U89915; AAC32982.1; -; mRNA.
DR   PDB; 1F97; X-ray; A=27-238.
DR   Ensembl; ENSMUSG00000038235; Mus musculus.
DR   MGI; MGI:1321398; F11r.
DR   GO; GO:0005923; C:tight junction; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007155; P:cell adhesion; IDA.
DR   GO; GO:0030855; P:epithelial cell differentiation; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   3D-structure; Glycoprotein; Immunoglobulin domain; Repeat; Signal;
KW   Tight junction; Transmembrane.
FT   SIGNAL   1   26   Potential.
FT   CHAIN   27   300   Junctional adhesion molecule A.
FT   TOPO_DOM   27   238   Extracellular (Potential).
FT   TRANSMEM   239   259   Potential.
FT   TOPO_DOM   260   299   Cytoplasmic (Potential).
FT   DOMAIN   28   122   Ig-like V-type 1.
FT   DOMAIN   134   230   Ig-like V-type 2.
FT   CARBOHYD   42   42   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   185   185   N-linked (GlcNAc...) (Potential).
FT   DISULFID   49   108   Potential.
FT   DISULFID   152   212   Potential.
FT   STRAND   29   31
FT   STRAND   36   40
FT   TURN   41   42
FT   STRAND   45   48
FT   STRAND   50   52
FT   STRAND   57   65
FT   TURN   66   67
FT   TURN   68   74
FT   STRAND   75   76
FT   TURN   77   78
FT   STRAND   80   82
FT   HELIX   83   85
FT   TURN   86   89
FT   STRAND   89   91
FT   TURN   90   91
FT   STRAND   92   95
FT   HELIX   100   102
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FT   STRAND      104    112
FT   TURN        113    114
FT   STRAND      118    129
FT   STRAND      135    137
FT   TURN        141    143
FT   STRAND      144    145
FT   TURN        148    153
FT   STRAND      158    158
FT   STRAND      162    167
FT   STRAND      168    169
FT   STRAND      170    171
FT   STRAND      173    173
FT   STRAND      181    181
FT   STRAND      188    190
FT   TURN        192    194
FT   TURN        197    199
FT   HELIX       204    206
FT   STRAND      208    215
FT   STRAND      222    223
FT   STRAND      227    232
SQ   SEQUENCE    300 AA;  32369 MW;  391F3E48FF3B97EC CRC64;

Query Match         68.1%;  Score 1073.5;  DB 1;  Length 300;
Best Local Similarity   69.5%;
Matches  205;  Conservative   44;  Mismatches   49;  Indels    3;  Gaps    3;
                                   Pred. No. 5.5e-75;

Qy    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEEPEVRIPENNPVKLSCAYSGFSSPRV   60
         |||:.||  ||:|:|.||:.|.|||| :||||:||||:|||||| ::|| | :|| || |||
Db    1  MGTEGKAGRLLFLF-TSMIGSLVQGKGSVYTAQSDVQPENESIKLTCTYSGFSSPRV      59

Qy   61  EWKFDQGGTTRLVCYNNKITASYEDRVTLFLPTGITFKSVTREDTGTYTCMVSEBGGNSYG  120
Db   61  EWKFVQGSTPALVCVNSQITAPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEBGGQNYG   119

Qy  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPT-NPKS   179
Db  120  EVSIHLTVLVPPSKPTISVPSSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKK  179

Qy  180  TRAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI  239
Db  180  TRAFMNSSFPIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGI   239

Qy  240  VAAVLVTLLLGILLVFGIWFAYSRGHFDRTKKGTS-SKKVIYSQPSARSEGEFKQTSSFL   298
Db  240  VAAVLVTLILGLLIFGWFAYSRGYFETTKKGTAPGKKVIYSQPSTRSEGEFKQTSSFL    299

Qy  299  .                                                             299
         |
Db  300  .                                                             300
```

RESULT 9

Q9JKD5_RAT

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ID   Q9JKD5_RAT     PRELIMINARY;     PRT;   173 AA.
AC   Q9JKD5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule (Fragment).
GN   Name=F11r;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
```

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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kirsch T., Wellner M., Haller H., Lippoldt A.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
```

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DR   EMBL; AF241261; AAF61729.1; -; mRNA.
DR   HSSP; O88792; 1F97.
DR   SMR; Q9JKD5; 1-111.
DR   RGD; 621842; F11r.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IG; 1.
DR   SMART; SM00409; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE    173 AA;  18706 MW;  3E33ECDFA5AFB8B2 CRC64;

Query Match         45.3%;  Score 700;  DB 2;  Length 173;
Best Local Similarity   79.8%;
Matches  138;  Conservative   16;  Mismatches   17;  Indels    2;  Gaps    2;
                                   Pred. No. 2.5e-46;

Qy  129  LVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPT-NPKSTRAFSNSS  187
         |||||||| .||||.|||||||||||:||||||||:||||| .|:| ||  ||||:|||
Db    1  LVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAFINSS   60

Qy  188  YVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTL  247
         | :   .| |||||.||.|:|||| ||:||||| | |||||||  |||| |||||||||
Db   61  YTIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAELNVGGIVAAVLVTL   120

Qy  248  ILLGILVFGIWFAYSRGHFDRTKKGTS-SKKVIYSQPSARSEGEFKQTSSFLV         299
         ||||:| ||||||||||.|:.||||| .|||||||||  |||||||||||||
Db  121  ILLGLLIFGIWFAYSRGYFERTKKGTAPGKKVIYSQPSQPSTRSEGEFKQTSSFLV      173
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RESULT 10

Q72WT0_XENLA

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ID   Q72WT0_XENLA     PRELIMINARY;     PRT;   289 AA.
AC   Q72WT0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC53721 protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
```

RC   TISSUE=Embryo;
RL   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046720; AAH46720.1; -; mRNA.
DR   HSSP; Q08792; 1F97.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Transmembrane.
SQ   SEQUENCE   289 AA;   31630 MW;   24354B5A3761B845 CRC64;

RESULT 11
ID   Q640C0_XENLA
AC   Q640C0;
Q640C0_XENLA PRELIMINARY;   PRT;   296 AA.

Query Match   39.0%; Score 602.5; DB 2; Length 289;
Best Local Similarity   43.7%; Pred. No. 1.7e-38;
Matches 129; Conservative 54; Mismatches 95; Indels 17; Gaps 8;

Qy   9 RKLICLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSG-FSSPRVEWKF-DQ 66
            |::|| ::: |||::||||||||||||||||::||||||||||| |::| ||||||| :|
Db   8 RRAVGVGLLCCCLWTVTLAAVT--TPNPTIIVKEGESAELCQCSYSDFTSPRVEWKFVNK 65

Qy   67 GDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNS-YGEVKVK 125
            ::||| | :| ::::|||||| | || |||| |::| || |||||||||||| || |||
Db   66 DQETSFVFYDGSLTAPYKDRAIPYPQGITLKQITRKDAGEYSCEVTSTGSKTLYGEAKIQ 125

Qy   126 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSN 185
            |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 LQVIVAPSKPVAQVPRSVSVSTGSVAELLCVENDGYPPPTFIWYRNKSPMQIAPQ----N 179

Qy   186 SSYVLNPTTGELVFDPLSASDTGEYSVSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLV 245
            || |||||||||||||||||||||:|||||||||||||||||||||||||||||:
Db   180 STYTIDPKTGVLKFAAVSTSDSGEYYCEATNNQG-KQASDLVRMDVQDVNVGGIVAAVVI 238

Qy   246 TLILGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS-ARSEGEFKQTSSFLV 299
            |||| |||||||||||||||| |:|||::||||||| ::||||||||||:||
Db   239 VLILALIGFGMWFAYSRGYLDRKE----NKKVIYSLPSETRSDKNFQQTSSFLV 289

RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse full-length cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC082710; AAH82710.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
NON_TER   1
FT   NON_TER   1
SQ   SEQUENCE   296 AA;   32269 MW;   2EF4953AB840A15C CRC64;

RESULT 12
ID   Q7SYQ7_XENLA
AC   Q7SYQ7;
Q7SYQ7_XENLA PRELIMINARY;   PRT;   300 AA.

Query Match   37.6%; Score 580.5; DB 2; Length 296;
Best Local Similarity   45.2%; Pred. No. 8.8e-37;
Matches 132; Conservative 46; Mismatches 93; Indels 21; Gaps 11;

Qy   16 ILAILLC----SLALGSVTVHSSEPEVRIPENNPVKLSCAY-SGFSSPRVEWKF-DQGDT 69
            ||:||| |||||||||||||||||||||||||||||| ||||||||||||| |
Db   18 LLAILCCCLWTVTLAAVT--APDFTIIVKEGDSPDLRCSYTSDYINPRVEWKFVNKDQE 75

Qy   70 TRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGN-SYGEVKVKLIV 128
            ||||||||||||||||||||||||:|| ||||||||||||:| ||| |:|| |||||:|
Db   76 TSFVFYDGSLTASYKDRATSYPQGIKLNQVTRKDAGEYSCEVTSTGTKVLYGEAKIQLQV 135

Qy   129 LVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSY 188
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   136 IVAPGTPVAQVPSSARTGSVAELMCVETQGFPLPTFIWYHNN--SPMQAKS----QNSTY 189

Qy   189 VLNPTTGELVFDPLSASDTGEYSVSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI 248
            ||||||||||||||||||||||:|||||||||||||||||||||:|||:||:|||||:|||
Db   190 TIDPNTGVLKFASVGISDSGBYYCKATNSQG-EQSSAIVRMDVKDVNVGGIVAAVVIVLL 248

Qy   249 LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS-ARSEGEFKQTSSFLV 299
            :||:||||||||||||:||| |:||:||||||||| ::|||||||||||||
Db   249 ILALLGFGLWFAYSRGYLDR--KG--NKKVIYSQSETRSDKNFQQTSSFLV 296

RA   Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RL Dev. Dyn. 225:384-391(2002).
DR EMBL; BC054305; AAH54305.1; -; mRNA.
DR HSSP; O88792; 1F97.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER   1   1
SQ SEQUENCE   300 AA; 32858 MW; 02BC49DC74E271D4 CRC64;

Query Match   37.6%; Score 580.5; DB 2; Length 300;
Best Local Similarity   45.2%; Pred. No. 9e-37;
Matches 132; Conservative   46; Mismatches   93; Indels   21; Gaps   11;

Qy   16 ILAILLC----SLALGSVTVHSSSEPEVRIPENNPVKLSCAY-SGFSSPRVEWKF-DQGDT 69
Db   22 LLALLCCCLWTAALLAGVT--APDPITVKEGDSPDLRCSYTSDYINPRVEWKFVNKDQE 79

Qy   70 TRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGN-SYGEVKVKLIV 128
Db   80 TSFVFYDGSLTASYKDRATSYPQGIKLNQVTRKDAGEYSCEVSTSGTKVLVYGEAKIQLQV 139

Qy   129 LVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSY 188
Db   140 IVAPGTPVAQVPSARTGSVABLMCVETQGFPLPFFTWYYNN----SPMQAKS----QNSTY 193

Qy   189 VLNPFTGELVPFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI 248
Db   194 TIDPNTGVLKFASVGTSDSGGEYYCKATNSGQ-EQSSAIVRMDVKDVNVGGIVAAVVIVLL 252

Qy   249 LIGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPS-ARSEGEREKQTSSFLV 299
Db   253 ILALLGFGLWFAYSRGYLDR--KG--NKKVIYSQPSETRSDXNFQQTSSFLV 300

RESULT 13
Q66172 BRARE
ID   Q66172_BRARE PRELIMINARY; PRT; 292 AA.
AC   Q66172;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   F11 receptor.
GN   Name=f11r;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Larvae;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C., Carninci P.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Larvae;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081502; AAH81502.1; -; mRNA.
DR   ZFIN; ZDB-GENE-030131-2416; f11r.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Receptor.
SQ   SEQUENCE   292 AA; 32091 MW; E1F6B5FE74A72502 CRC64;

Query Match   37.0%; Score 571.5; DB 2; Length 292;
Best Local Similarity   44.4%; Pred. No. 4.3e-36;
Matches 123; Conservative   38; Mismatches 105; Indels   11; Gaps   6;

Qy   29 VTVHSSSEPEVRIPENNPVKLSCAY-SGF-SSPRVEWKF-DQGDTTRLVCYNNKITASYED 85
Db   21 VTVTS---PVKVKENEGVDLQCSYTSDFGATPRVEWKFKDLKGSQTLVYFDGKPTQYTG 77

Qy   86 RVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATI 145
Db   78 RVTMYDKGLRNKVTRADTGDYDCEVSGSGSGG--YGENTIKLTVLVPPAKPVSRIPSSVTT 135

Qy   146 GNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPFTGELVPFDPLSAS 205
Db   136 SSNVRLTCFDPVGSPPSTYKWKDNTPLPEDTKFPAFKNLTYKMNVFNGNLEFPSVSKM 195

Qy   206 DTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSRGH 265
Db   196 DTGSYFCEASNGEGVPQRGDEVKMEVRDLNVGGIVAGVIVALLAVGLLLFGLWYASKGGY 255

Qy   266 FDRTKKGTSSSKKVIYSQPSARSEGE---FKQTSSFLV 299
Db   256 LPKLSETKQKPQAVTQPQTDDVDEANGFRQKSSFVV 292

```
RESULT 14
Q66JT5_XENTR
ID   Q66JT5_XENTR    PRT;   291 AA.
AC   Q66JT5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MGC79514 protein.
GN   Name=MGC79514;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR   EMBL; BC080901; AAH80901.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   291 AA;   31538 MW;   D6A11S178E222A6 CRC64;

Query Match      36.3%;  Score 560.5; DB 2; Length 291;
Best Local Similarity   40.9%;  Pred. No. 3.1e-35;
Matches  123;  Conservative  54;  Mismatches 105;  Indels  19;  Gaps  9;

Qy   5 AQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY-SGFSSPRVEWK 63
         ||::   | ||  ||| | |||   ||  :|:|||||| ||||||  | ::| ||| ||||
Db   4 ASSNRGAVVLGLLCACLWTAAPAGVS--TPNPTITVKQGATADLRCTYTSDFTKSRVEWK 61

Qy  64 FDQGD-TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEBGGNS---Y 119
         | |:  ::| ||| |  |||| |||| |||||||||||||||||||| |||  |||    |
Db  62 FVNNQLETFVYYDGTLTASYVNRATSVPQGIILNQITSKDAGEYSCEVTSVDSNCQTLY 121

Qy 120 GEVKKIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKS 179
         || |  ||| |||  ||  |||  || ||| |||| |:|| | || |  |:|  ||:
Db 122 GEAKIQLLVIVAPSQPMAHVENTVRGSAVELRCVETQGYGPPTFTWYQNKAPMPENPQ- 180

Qy 180 TRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVI 239
         |  ::|  |::|| ||  | |  |  ||| ||| |   : : |  |||||| |  :| |||
Db 181 ----NATYTIDPNTGVLKFRAVAASDSGDYCKAANSEG-EQVSAIVRMNVQDVAVGGI 234

Qy 240 VAAVLVTLILLGIIVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS-ARSEGEFKQTSSFL 298
         |||::| |||  |:| |:| ||||| :| || ::|| ::|||||| :||| | |||||||
Db 235 VAAVIVLLILALIGFGLWYAYSRGYLD--KKG--NKVIYSQPSETRSDKNFQQTSSFL 290

Qy 299 V 299
         |
Db 291 V 291
```

```
RESULT 15
Q4S8Z8_TETNG
ID   Q4S8Z8_TETNG    PRT;   260 AA.
AC   Q4S8Z8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 7 SCAF14703, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00022119001;
OS   Tetraodon nigroviridis (Green pufferi).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014703; CAG02884.1; -; Genomic_DNA.
NON_TER     260
NON_TER     260
SQ   SEQUENCE   260 AA;   28017 MW;   7D8EA67FCA13CAF7 CRC64;

Query Match      34.6%;  Score 534.5; DB 2; Length 260;
Best Local Similarity   42.6%;  Pred. No. 2.8e-33;
Matches  110;  Conservative  42;  Mismatches  99;  Indels  7;  Gaps  4;

Qy  12 LCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSP--RVEWKFD--QG 67
         |  | || |  |:| ||  |  :|:| |||||:  | |||:|| |:|   ||| ||   |
Db   5 VAWWAAAFLLSATGVCGPSVTTEKSEVEVGENNGVDLICTYSADFGPNARVEWKFKNLQG 64

Qy  68 DTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEBGGNSYGEVKVKLI 127
         :  | |||| |  ||| |:|  |  |  |  ||| |||   |:| | |:| |  |:|:| :
Db  65 SQVYVV-FDGKPTEPYSSRLTMYNSNLRFSKVTRKDNGVFDCEVS--GNGQFQEVRVLT 121

Qy 128 VLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSS 187
         |||||| | ||||| |: | ||| |||  |:|||| | ||  |||  |:||:|   :  :
Db 122 VLVPPSPVCNIPSSVTTGGRATLDCNDPDGSPPPTYRWYKNGVPLPADPSKISGYQNAT 181

Qy 188 YVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTL 247
         | |:| |  | |  |:|| ||||:||| |  | |  |||||| | |::| ||||| :| |
Db 182 YSLDTELGKLTYSKTSLSDSGEYFCEAVNKAGPAQRCRAVRMEVRDLNTGGIVAGVIVAL 241
```

```
Qy   248  ILLGILVFGIWPAYSRGH  265
          :|| :|||||||:| :|:
Db   242  LLLALLVFGIWYANKKGY  259
```

Search completed: May 16, 2006, 07:07:42
Job time : 271 secs

OM protein - protein search, using sw model

GenCore version 5.1.8

Run on: May 16, 2006, 07:01:24 ; Search time 40 Seconds
(without alignments)
719.220 Million cell updates/sec

Title: US-10-785-433-1
Perfect score: 1544
Sequence: 1 MGTKAQVERKLLCLFILAIL.........YSQPSARSEGEFKQTSSFLV 299

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 283416
Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1544	100.0	299	2	S56749	junctional adhesio
2	196	12.7	365	2	JC7780	coxsackie- and ade
3	189.5	12.3	7962	2	I38346	elastic titin - hu
4	181.5	11.8	862	2	I49583	differentiation an
5	181.5	11.8	868	2	A46512	CD22 homolog/B lym
6	179	11.6	538	2	JC2457	vascular cell adhe
7	178.5	11.6	847	2	JH0371	B-cell adhesion pr
8	178	11.5	483	2	T17346	hypothetical prote
9	177.5	11.5	647	2	A35648	B-cell adhesion pr
10	177.5	11.5	1273	2	T42405	sax-3 protein - Ca
11	172.5	11.2	1227	2	T23004	hypothetical prote
12	171	11.1	1091	2	A58532	cell adhesion mole
13	169.5	11.0	765	2	C42632	glial cell membran
14	169.5	11.0	812	2	B42632	cell adhesion mole
15	169.5	11.0	932	2	A42632	cell adhesion mole
16	169.5	11.0	2222	2	T13924	sdk protein - frui
17	169	10.9	739	2	JN0581	vascular cell adhe
18	167.5	10.8	423	2	T29549	hypothetical prote
19	167.5	10.8	1896	2	T08851	Down syndrome cell
20	167	10.8	584	2	T08678	hypothetical prote
21	166	10.8	5175	2	T20992	hypothetical prote
22	166	10.8	5198	2	S01998	hemicentin precurs
23	165.5	10.7	4162	2	T42633	connectin/titin -
24	165	10.7	344	2	A27681	nonspecific cross-
25	165	10.7	6642	2	T29757	protein UNC-89 - C
26	163.5	10.6	875	2	T33434	hypothetical prote
27	160	10.4	1051	2	A39712	kinase-like protei
28	160	10.4	1328	2	T23007	hypothetical prote
29	158	10.2	1040	2	A49356	transient axonal g
30	157.5	10.2	1091	1	IJCHNL	neural cell adhesi
31	157.5	10.2	725	1	JE0099	neural cell adhesi
32	157.5	10.2	1088	1	IJXLNL	neural cell adhesi
33	157	10.2	1323	2	PN0568	connection 3B - chi
34	156	10.1	1199	2	T23005	hypothetical prote
35	156	10.1	1015	2	T32186	hypothetical prote
36	156	10.1	1040	2	A34695	axonal glycoprotei
37	155.5	10.1	521	2	S34338	biliary glycoprote
38	155.5	10.1	799	2	S18209	fibroblast growth
39	155.5	10.1	858	1	ICRTNC	vascular cell adhe
40	155	10.0	1499	2	I50212	protein-tyrosine k
41	155	10.0	1070	2	JC4593	neural cell adhesi
42	154	10.0	739	2	JS0675	protein-tyrosine-p
43	154	10.0	1256	2	TO3096	vascular cell adhe
44	153.5	10.0	853	2	ICBONC	CDO protein - rat
45	153	9.9	1036	2	S22383	neural cell adhesi
46	153	9.9	344	2	I56551	neurotrimin - rat
47	153	9.9	1257	1	I41060	neuroglian - fruit
48	153	9.9	1239	2	A32579	neural cell adhesi
49	153	9.9	1260	1	I50600	protein-tyrosine k
50	153	9.9	1338	2	JC4776	limbic-system-asso
51	152	9.8	338	2	S22383	axonin 1 precursor
52	152	9.8	1257	1	I56551	neural cell adhesi
53	152	9.8	1115	2	I41060	neurotrimin - rat
54	151.5	9.8	3707	2	S18252	neurogenin - chicken
55	151.5	9.8	458	2	JC1509	biliary glycoprote
56	151.5	9.8	1115	2	LIMSNL	neural cell adhesi
57	151.5	9.8	3707	2	S18252	neural cell adhesi
58	150.5	9.7	265	2	A55811	heparan sulfate pr
59	150.5	9.7	349	2	A34815	carcinoembryonic a
60	150.5	9.7	521	2	JC1508	carcinoembryonic a
61	150.5	9.7	1033	2	S19247	biliary glycoprote
62	150.5	9.7	1501	2	I58148	cell adhesion prot
63	150.5	9.7	1863	2	S46217	protein-tyrosine-p
64	150	9.7	702	2	A36319	protein-tyrosine-p
65	150	9.7	2783	2	T34416	carcinoembryonic a
66	149.5	9.7	725	2	JE0100	hypothetical prote
67	149.5	9.7	1907	2	S50093	neural cell adhesi
68	149	9.7	526	2	A32164	neural cell adhesi
69	149	9.7	647	2	A41288	fibroblast growth
70	149	9.6	739	2	A41288	perlecan precursor
71	148	9.6	650	2	JC1450	protein-tyrosine k
72	148	9.6	1021	2	I39207	protein-tyrosine-p
73	148	9.6	1612	2	T30805	protein-tyrosine k
74	148	9.6	946	1	A47299	protein-tyrosine-p
75	147.5	9.6	1092	2	JN0635	vascular cell adhe
76	147.5	9.6	333	1	A31923	leukocyte antigen-
77	147	9.5	458	1	WMMSR1	rig-1 protein - mo
78	146.5	9.5	1694	2	S50065	ecto-ATPase precur
79	146.5	9.5	1259	2	S36126	leukocyte antigen-
80	146	9.4	4391	2	A38096	Fit-1 tyrosine kin
81	145	9.4	802	1	TVHUF4	biliary glycoprote
82	145	9.4	871	1	I48696	protein-tyrosine-p
83	145	9.4	881	2	I48697	amalgam protein -
84	145	9.4	341	2	A56178	neural cell adhesi
85	145	9.4	1912	2	A56178	ror-related recept
86	144.5	9.4	946	2	I60598	leukocyte surface
87	144.5	9.4	1897	1	TDHULK	duttl protein - mo
88	144.5	9.3	519	2	A44783	fibroblast growth
89	144	9.3	1344	2	T14316	vascular cell adhe
90	144	9.3	1898	2	S46216	vascular cell adhe
91	143	9.3	206	2	A40305	biliary glycoprote
92	143	9.3	286	2	A28333	heparan sulfate pr
93	143	9.3	509	2	JC5288	neural cell adhesi
94	143	9.3	513	2	JC5289	biliary glycoprote
95	143	9.3	1091	2	S01998	SHP substrate-1 pr
96	143	9.3	1277	2	T30532	contactin precurso
97	143	9.2	1277	1	I38344	neural cell adhesi
98	142.5	9.2	26926	1	26926	titin, cardiac mus
99	142.5	9.2	278	1	A39037	carcinoembryonic a
100	142.5	9.2	1262	2	B48758	protein-tyrosine-p
101	142	9.2	1496	2	A48758	carcinoembryonic-p
102	142	9.2	351	2	JH0396	biliary glycoprote

103	142	9.2	417	2	JH0394	biliary glycoprote
104	142	9.2	464	2	C30127	transmembrane carc
105	142	9.2	976	2	T29583	hypothetical prote
106	141.5	9.2	338	2	JC5519	50K glycoprotein p
107	141.5	9.2	567	2	S29498	lymphocyte antigen
108	141.5	9.2	626	1	A61084	myelin-associated
109	141.5	9.2	1651	2	T14160	transmembrane rece
110	141.5	9.2	1894	2	C54689	protein-tyrosine-p
111	141	9.1	882	2	I38912	receptor tyrosine
112	140.5	9.1	278	2	JC1506	biliary glycoprote
113	140.5	9.1	577	2	I50731	biliary glycoprote
114	140.5	9.1	811	2	A41054	Ig heavy chain - n
115	140.5	9.1	873	2	B41054	fasciclin II, tran
116	140.5	9.1	1240	2	T03097	fasciclin II pi-li
117	140.5	9.1	1348	2	S51656	CDO protein - huma
118	140	9.1	890	2	A53743	vascular endotheli
119	140	9.0	1020	2	S05944	protein-tyrosine k
120	138.5	9.0	335	2	C54312	neuronal cell surf
121	138.5	9.0	335	2	B33251	pregnancy-specific
122	138	8.9	880	2	B53743	nonspecific cross-
123	138	8.9	1021	2	A57112	protein-tyrosine k
124	138	8.9	335	2	A33514	contactin precurso
125	137.5	8.9	341	2	JC1511	pregnancy-specific
126	137.5	8.9	518	2	JC1511	biliary glycoprote
127	137.5	8.9	2295	2	C88369	poliovirus recepto
128	137	8.9	582	2	BNRT3S	protein unc-52 [im
129	137	8.9	626	1	BNRT3	myelin-associated
130	137	8.9	637	2	B33785	myelin-associated
131	137	8.9	816	2	A49151	myelin-associated
132	137	8.9	1333	2	I78875	receptor tyrosine
133	137	8.9	1535	2	S46224	peroxidasin - frui
134	136.5	8.9	273	2	A29915	teratocarcinoma gl
135	136.5	8.8	330	2	B28928	pregnancy-specific
136	136.5	8.8	345	2	S03199	opioid-binding pro
137	136.5	8.8	713	2	I50128	fibroblast growth
138	136.5	8.8	3375	2	T19821	hypothetical prote
139	136	8.8	707	2	A54846	fibroblast growth
140	135.5	8.8	832	2	JH0393	protein-tyrosine k
141	135.5	8.8	1367	2	A41228	fibroblast growth
142	135	8.7	235	2	S20000	Ig light chain pre
143	135	8.7	880	1	JC4166	protein-tyrosine k
144	134.5	8.7	275	2	A28928	pregnancy-specific
145	134.5	8.7	282	2	C28928	pregnancy-specific
146	134.5	8.7	395	2	D43354	pregnancy-specific
147	134.5	8.7	397	2	C43354	pregnancy-specific
148	134.5	8.7	406	2	E43354	pregnancy-specific
149	134.5	8.7	417	2	A28277	pregnancy-specific
150	134.5	8.7	426	2	A35964	pregnancy-specific
151	134.5	8.7	818	2	S44098	brain-derived neur
152	134.5	8.7	822	1	TVMSFG	fibroblast growth
153	134.5	8.7	1028	2	A53449	plasmacytoma-assoc
154	134.5	8.7	1330	2	S49010	embryonic receptor
155	134.5	8.7	1880	2	T18531	tractin - medicina
156	134	8.7	458	2	S68177	C-CAM2a protein is
157	134	8.7	458	2	S23969	cell-adhesion mole
158	134	8.7	588	2	I37202	B-CAM protein - hu
159	134	8.7	628	2	I38000	Lutheran blood gro
160	134	8.7	919	1	T32541	unc-5 protein, Ion
161	134	8.7	947	1	B44294	unc-5 protein - Ca
162	133.5	8.7	278	2	JC1507	biliary glycoprote
163	133.5	8.6	419	2	A33258	pregnancy-specific
164	133.5	8.6	419	2	A31135	pregnancy-specific
165	133.5	8.6	426	2	B33258	pregnancy-specific
166	133.5	8.6	426	2	A35341	pregnancy-specific
167	133.5	8.6	428	2	A27658	pregnancy-specific
168	133.5	8.6	687	2	A49636	soluble vascular e
169	133.5	8.6	729	2	A56795	fibroblast growth
170	133.5	8.6	428	2	I57486	fibroblast growth
171	133	8.6	428	2	JS0032	pregnancy-specific
172	133	8.6	1021	2	T42634	connectin/titin -
173	132.5	8.6	822	2	S29840	fibroblast growth
174	132	8.5	345	2	JC4025	opioid-binding cel
175	132	8.5	345	2	JC1239	opioid-binding pro

176	132	8.5	707	2	A38429	keratinocyte growt
177	132	8.5	1018	2	A54744	contactin 1 precur
178	132	8.5	1018	2	JC4211	neural adhesion pr
179	131.5	8.5	419	2	S43312	neural cell adhesi
180	131.5	8.5	419	2	A36109	pregnancy-specific
181	131.5	8.5	733	2	I49293	fibroblast growth
182	131.5	8.5	822	2	I49289	fibroblast growth
183	131.5	8.5	1265	2	A37967	neural cell adhesi
184	131.5	8.5	2029	1	TDFFLK	protein-tyrosine-p
185	130.5	8.5	1	2	T22098	hypothetical prote
186	130.5	8.5	304	1	RWCHH7	cell surface glyco
187	130.5	8.5	338	2	JC1238	opioid-binding pro
188	130.5	8.5	435	2	D33258	pregnancy-specific
189	130.5	8.5	1011	2	T13669	neuromusculin - fr
190	130	8.4	166	2	A33402	pregnancy-specific
191	130	8.4	520	1	S44099	brain-derived neur
192	129.5	8.4	309	2	I49503	B-lymphocyte activ
193	129.5	8.4	392	1	RWHUPD	poliovirus recepto
194	129.5	8.4	417	2	RWHUPA	poliovirus recepto
195	129.5	8.4	662	2	C40862	heparin-binding gr
196	129.5	8.4	822	1	TVHUFG	fibroblast growth
197	129.5	8.4	822	2	B49151	fibroblast growth
198	129.5	8.4	1173	2	T25893	biliary glycoprote
199	129	8.4	876	2	I49152	hypothetical prote
200	129	8.4	1427	2	I51669	protein-tyrosine k
201	128	8.3	823	2	S15674	tumor suppressor -
202	128	8.3	823	2	B35963	cell surface glyco
203	128	8.3	424	2	A34595	protein-tyrosine k
204	128	8.3	416	2	S19947	poliovirus recepto
205	127.5	8.3	898	2	A40114	fasciclin II precu
206	127.5	8.3	353	2	A42879	fibroblast growth
207	127.5	8.3	709	2	A35364	heparin-binding fi
208	127	8.2	416	1	A42879	advanced glycosyla
209	127	8.2	1197	2	T30581	carcinoembryonic a
210	127	8.2	271	2	S43512	GP42/Basigin prote
211	126.5	8.2	272	1	I48268	platelet-derived g
212	126.5	8.2	273	2	JX0107	billiary glycoprote
213	126.5	8.2	824	2	S24108	basigin precursor
214	126.5	8.2	1232	2	T43027	protein-tyrosine k
215	126.5	8.2	1447	2	A54100	neural cell adhesi
216	126.5	8.2	275	2	PS0402	tumor suppressor P
217	126	8.2	374	2	S69339	basigin type III -
218	126	8.2	475	2	A54879	Ig heavy chain V r
219	126	8.2	789	2	T28714	pregnancy-specific
220	126	8.2	1355	2	T28715	hypothetical prote
221	126	8.2	1356	2	JC1402	hypothetical prote
222	126	8.2	398	2	S17428	protein-tyrosine k
223	125.5	8.1	398	2	JC4123	interleukin-1 rece
224	125.5	8.1	495	2	A55181	pregnancy-specific
225	125.5	8.1	495	2	TVHUF2	pregnancy-specific
226	125.5	8.1	821	2	I58164	fibroblast growth
227	125.5	8.1	1028	2	A43425	BIG-1 protein - ra
228	125.5	8.1	1259	2	A39640	Bravo/Nr-CAM cell
229	125	8.1	1268	1	PS0402	neural cell adhesi
230	125	8.1	530	2	A53437	poliovirus recepto
231	124.5	8.1	233	2	I51383	Ig lambda chain -
232	124.5	8.1	413	2	S65948	hemolin - cecropia
233	124.5	8.1	769	1	QRRTGS	secretory componen
234	124.5	8.1	819	1	TVCHFG	fibroblast growth
235	124.5	8.1	917	2	I48950	telencephalin prec
236	124	8.0	917	2	A35969	heparin-binding gr
237	124	8.0	769	2	S16236	fibroblast growth
238	124	8.0	822	2	A45081	keratinocyte growt
239	124	8.0	822	2	A41794	fibroblast growth
240	124	8.0	182	2	I83053	pregnancy-specific
241	123.5	8.0	503	2	JC5287	SHP substrate-1 pr
242	123.5	8.0	523	2	I50478	pregnancy-specific
243	123.5	8.0	797	2	S38579	neurolin - goldfis
244	123.5	8.0	1209	2	T42718	fibroblast growth
245	123	8.0	812	1	A36477	probable neural ce
246	122.5	7.9	1209	2	I46690	CD80 precursor r
247	122.5	7.9	299	2	C27658	pregnancy-specific
248	122.5	7.9	336	2	B36109	pregnancy-specific

No.					Accession	Description
249	122.5	7.9	646	2	I38049	cell surface glyco
250	122	7.9	243	2	A52244	leukocyte antigen
251	122	7.9	1375	2	T13822	frazzled gene prot
252	122	7.9	1526	2	T13823	frazzled gene prot
253	121.5	7.9	233	2	S29577	Ig light chain - r
254	121.5	7.9	255	2	JC7593	SH2 domain-contain
255	121.5	7.9	318	2	P72171	K9R protein - vari
256	121.5	7.9	404	1	161596	advanced glycosyla
257	121.5	7.9	1471	2	T19506	hypothetical prote
258	121	7.8	275	2	H35216	FP31 protein - fow
259	121	7.8	402	2	T09062	probable advanced
260	121	7.8	818	2	T19120	hypothetical prote
261	121	7.8	822	2	B54846	fibroblast growth
262	121	7.8	1437	2	T31093	probable protein-t
263	119.5	7.8	257	2	PS0401	basigin type II -
264	119.5	7.7	352	2	I77374	pregnancy-specific
265	119.5	7.7	960	1	JN0677	protein-tyrosine k
266	119	7.7	212	2	C33258	pregnancy-specific
267	118.5	7.7	352	2	JH0593	Schwann cell myeli
268	118.5	7.7	524	2	T33433	hypothetical prote
269	118	7.6	225	2	S35341	kettin - fruit fly
270	118	7.6	253	2	I51335	Ig lambda chain -
271	118	7.6	421	2	T15475	hypothetical prote
272	118	7.6	426	2	T46266	hypothetical prote
273	118	7.6	620	2	S09016	Schwann cell myeli
274	118	7.6	773	2	T46283	fibroblast growth
275	117.5	7.6	806	2	TVHUF3	protein-tyrosine k
276	117.5	7.6	806	2	A35963	fibroblast growth
277	118	7.6	814	1	A39752	fibroblast growth
278	117.5	7.6	328	2	S30444	ST2 protein - huma
279	117.5	7.6	467	1	HLMSP3	poliovirus recepto
280	117.5	7.6	538	1	I68093	PR2 delta - human
281	117.5	7.6	764	1	QRHUGS	secretory componen
282	117.5	7.6	1089	1	PFHUGA	platelet-derived g
283	117.5	7.6	1089	1	S33727	platelet-derived g
284	117.5	7.6	232	2	S25756	Ig lambda chain -
285	117	7.6	330	2	I46691	CD86 precursor - r
286	117	7.6	480	2	B56182	fibroblast growth
287	117	7.6	508	2	A33378	fasciclin III prec
288	116.5	7.5	240	2	JL0143	antigen BCM1 precu
289	116.5	7.5	267	2	A38442	probable tumor sup
290	116.5	7.5	361	2	PN0020	fibroblast growth
291	116.5	7.5	800	2	A48991	heparin-binding gr
292	116	7.5	801	2	I55363	hypothetical prote
293	116	7.5	436	2	B55181	fibroblast growth
294	116	7.5	475	2	I76668	pregnancy-specific
295	116	7.5	705	2	S51635	fibroblast growth
296	116	7.5	2109	1	I50421	aggrecan precursor
297	115.5	7.5	238	2	C90909	probable major tal
298	115.5	7.5	426	2	C55181	pregnancy-specific
299	115.5	7.5	426	2	B35334	pregnancy-specific
300	115.5	7.5	495	2	T25750	hypothetical prote
301	115.5	7.5	800	1	TVHU2F	fibroblast growth
302	114.5	7.4	235	2	S25749	Ig lambda chain -
303	114.5	7.4	772	1	T13078	KIAA0092 protein -
304	114.5	7.4	820	2	S17295	fibroblast growth
305	114	7.4	336	2	S42632	Flt-18 protein pre
306	114	7.4	392	2	B44194	poliovirus recepto
307	114	7.4	417	2	A44194	poliovirus recepto
308	114	7.4	480	2	A55182	fibroblast growth
309	114	7.4	1272	2	S26180	neurofascin - chic
310	114	7.4	6831	2	A88852	protein unc-22 [im
311	114	7.4	6839	2	S57242	twitchin [similari
312	114	7.4	7160	2	T27935	hypothetical prote
313	113.5	7.4	321	2	I54756	B-lymphocyte activ
314	113.5	7.4	588	2	JH0506	adhesion molecule
315	113.5	7.4	588	2	A45254	surface glycoprote
316	113	7.3	313	2	T28598	hypothetical prote
317	113	7.3	748	2	S41050	fibroblast growth
318	112.5	7.3	259	2	JC7109	ST2V protein - hum
319	112.5	7.3	332	2	JN0067	pregnancy-specific
320	112.5	7.3	477	2	A34368	interferon gamma r
321	112.5	7.3	1906	1	S68235	myosin-light-chain
322	112	7.3	750	2	S41051	fibroblast growth
323	112	7.3	987	2	A88746	protein C18F3.2 [i
324	112	7.3	1287	2	T30988	hypothetical prote
325	112	7.3	1450	2	A44027	165K myofibrillar
326	111.5	7.2	821	1	TVMSBK	fibroblast growth
327	111.5	7.2	3488	2	T34418	hypothetical prote
328	111	7.2	313	2	JQ1862	31R protein - vari
329	111	7.2	860	2	JC5702	ErbB kinase activa
330	111	7.2	868	2	JC5701	ErbB kinase activa
331	110.5	7.2	232	2	S25702	Ig lambda chain pr
332	110.5	7.2	232	2	S17399	ErbB kinase activa
333	110.5	7.2	738	2	S25747	platelet-endotheli
334	110.5	7.2	813	1	A40096	fibroblast growth
335	110.5	7.2	2051	2	A49123	receptor tyrosine
336	110.5	7.2	6658	1	T30938	projection - fruit
337	110	7.1	213	2	T13931	Ig light chain pre
338	110	7.1	304	2	A21177	protein C18F3.3 [i
339	110	7.1	822	2	B88746	receptor tyrosine
340	110	7.1	1040	2	A56853	protein-tyrosine k
341	109.5	7.1	1103	2	A57638	MHC class I Lero-G
342	109.5	7.1	1052	2	T22889	hemolin precursor
343	109.5	7.1	353	2	G02922	brain-derived neur
344	109.5	7.1	413	2	A37778	hypothetical prote
345	109.5	7.1	477	1	I73631	brain-derived neur
346	109.5	7.1	618	2	T08685	c-kit-related kina
347	109.5	7.1	822	2	B49120	pregnancy-specific
348	109.5	7.1	954	2	S24600	p53 specific singl
349	109	7.1	269	2	A46506	pregnancy-specific
350	109	7.1	402	2	A54312	calcium vector pro
351	108.5	7.1	233	2	JC5322	c-kit-related kina
352	108.5	7.1	240	2	JC4121	Ig heavy chain pre
353	108.5	7.1	243	2	A37982	protein-tyrosine k
354	108.5	7.1	470	2	S22080	brain-derived neur
355	108.5	7.0	476	1	A35104	DM-GRASP precursor
356	108.5	7.0	587	2	B36182	OX-45 membrane gly
357	108	7.0	240	2	I58375	protein-tyrosine-p
358	108	7.0	612	2	T15746	s-glicerin precurs
359	108	7.0	773	1	A40985	irregular chiasm C
360	108	7.0	825	2	I73632	nerve growth facto
361	108	7.0	839	1	A55178	secretory componen
362	108	6.9	940	2	I73633	neurotrophin recep
363	108	6.9	964	2	S06943	neurotrophin-3 rec
364	108	6.9	1363	2	JH0464	projection - fruit
365	108	6.9	1462	2	S01299	hypothetical prote
366	108	6.9	240	2	I50419	protein-tyrosine k
367	107.5	6.9	584	2	A49448	Ig heavy chain pre
368	107.5	6.9	764	2	TVRTTB	fibroblast growth
369	107.5	6.9	799	1	T29340	myosin-binding pro
370	107.5	7.0	2541	2	T23555	brain-derived neur
371	107	6.9	268	2	S12839	brain-derived neur
372	107	6.9	380	2	JC4583	brain-derived neur
373	107	6.9	829	2	S56845	protein-tyrosine k
374	107	6.9	1142	2	C39667	hypothetical prote
375	107	6.9	474	1	B39667	PR2 alpha - human
376	106.5	6.9	476	2	A39627	brain-derived neur
377	106.5	6.9	790	2	A39667	hypothetical prote
378	106.5	6.9	821	2	C85630	ErbB kinase activa
379	106	6.9	259	2	I53960	protein-tyrosine k
380	106	6.9	478	2	JC5700	Ig lambda chain -
381	106	6.9	850	2	A48999	OX-2 membrane glyc
382	106	6.8	1298	2	S25748	pregnancy-specific
383	105.5	6.8	233	2	A47639	pregnancy-specific
384	105.5	6.8	274	2	G43354	pregnancy-specific
385	105.5	6.8	324	2	F43354	pregnancy-specific
386	105.5	6.8	326	2	A43354	pregnancy-specific
387	105.5	6.8	333	2	H43354	pregnancy-specific
388	105.5	6.8	335	2	S70587	butyrophilin precu
389	105.5	6.8	526	2	S25705	Ig mu chain - shee
390	105.5	6.8	592	2	I45956	polymeric immunogl
391	105.5	6.8	757	2	I45956	H-2 class II histo
392	105	6.8	253	2	S25687	probable major tal
393	105	6.8	281	2	H90853	probable major tal
394	105	6.8	310	2	JL0119	Fc gamma (IgG) rec

SEQ	Score		Length	N	Accession	Protein
395	105	6.8	317	2	JL0118	Fc gamma (IgG) rec
396	105	6.8	351	2	B34595	pregnancy-specific
397	105	6.8	874	2	T29548	hypothetical prote
398	105	6.8	1000	2	I46521	titin - rabbit (fr
399	105	6.8	6805	2	S20901	titin - rabbit (fr
400	104.5	6.8	230	2	S49449	Ig light chain -
401	104.5	6.8	240	2	A41797	Ig lambda chain - s
402	104.5	6.8	309	2	I49522	gene B7-2 protein
403	104.5	6.8	474	2	I50830	Ig mu chain - lepi
404	104.5	6.8	818	2	JC4058	fibroblast growth
405	104.5	6.8	824	2	S36439	fibroblast growth
406	104.5	6.8	1451	2	S42167	190K protein - hum
407	104.5	6.8	1599	2	T16210	hypothetical prote
408	104	6.7	238	2	A49633	Ig lambda-like cha
409	104	6.7	666	2	H89581	protein dim-1 [imp
410	104	6.7	1367	2	S48478	glucan 1,4-alpha-g
411	103.5	6.7	261	2	C85681	hypothetical prote
412	103	6.7	228	2	S29575	Ig light chain - r
413	103	6.7	238	2	E90822	probable major tai
414	103	6.7	313	2	H36854	hemagglutinin - va
415	103	6.7	1088	1	PFRTGA	platelet-derived g
416	102.5	6.7	547	2	T25478	hypothetical prote
417	102	6.6	167	2	S29579	Ig light chain - r
418	102	6.6	210	2	JC4122	pregnancy-specific
419	102	6.6	326	2	JC4124	pregnancy-specific
420	102	6.6	629	2	A46500	Ly-9.2 antigen - m
421	102	6.6	999	2	I38547	novel cellular pro
422	101.5	6.6	416	2	S33473	interleukin-1 rece
423	101.5	6.6	279	2	A47171	chondroitin sulfat
424	101.5	6.6	279	2	S04693	T-cell receptor de
425	101	6.5	323	2	S06946	hemagglutinin prec
426	101	6.5	757	1	S48841	Fc gamma (IgG) rec
427	101	6.5	976	2	TVHUKT	secretory componen
428	101	6.5	977	2	I45877	protein-tyrosine k
429	101	6.5	1518	2	S37928	probable purine nu
430	100.5	6.5	181	2	PT0220	Ig lambda chain V-
431	100.5	6.5	233	2	S25752	Ig lambda chain -
432	100.5	6.5	249	1	A61087	myelin P0 glycopro
433	100.5	6.5	315	2	HNVZVT	hemagglutinin prec
434	100.5	6.5	725	2	E86790	hypothetical prote
435	100	6.5	270	2	S65739	basigin precursor
436	100	6.5	662	2	T16525	hypothetical prote
437	99.5	6.4	135	2	S57892	T cell protein WI
438	99.5	6.4	140	1	A34509	Ig light chain C r
439	99.5	6.4	266	2	HLHU3D	MHC class II histo
440	99	6.4	226	2	S25745	Ig lambda chain -
441	99	6.4	238	2	D90876	major tail protein
442	99	6.4	262	2	C85692	probable tail comp
443	99	6.4	825	1	A40026	neurotrophin-3 rec
444	98.5	6.4	235	2	S05270	Ig lambda chain pr
445	98.5	6.4	278	1	TDRTOX	OX-2 membrane glyc
446	98.5	6.4	473	2	A56175	adhesive plaque pr
447	98.5	6.4	544	2	JC5018	intercellular adhe
448	98.5	6.4	729	2	A49120	fibroblast growth
449	98.5	6.4	942	2	JQ1674	protein kinase TMK
450	98.5	6.4	1379	2	JC4954	vascular endotheli
451	98.5	6.4	1398	2	T25568	hypothetical prote
452	98	6.3	176	2	I50016	MHC class I protei
453	98	6.3	213	2	S21066	Ig lambda chain V
454	98	6.3	235	2	S25754	Ig lambda chain -
455	98	6.3	290	1	F42527	B16R protein - vac
456	98	6.3	980	1	TVCTMD	macrophage colony-
457	98	6.3	983	2	B45583	receptor tyrosine
458	98	6.3	1123	2	S36846	myosin-binding pro
459	98	6.3	1138	2	S24614	myosin-binding pro
460	97.5	6.3	208	2	B49444	Ig lambda chain (N
461	97.5	6.3	235	2	S25750	Ig lambda chain -
462	97.5	6.3	266	1	HLHU4D	MHC class II histo
463	97.5	6.3	1241	2	T37190	nephrin - human
464	97	6.3	261	2	I48645	cell adhesion mole
465	97	6.3	330	2	A40071	Fc gamma (IgG) rec
466	97	6.3	330	2	I49660	Fc-gamma-1/gamma-2
467	97	6.3	370	2	S29139	aggrecan - pig (fr
468	97	6.3	487	2	T28804	hypothetical prote
469	97	6.3	504	2	S00390	Ig gamma chain (cl
470	96.5	6.2	516	2	S29258	Ig lambda chain V
471	96.5	6.2	233	1	FCMSG1	Fc gamma (IgG) rec
472	96.5	6.2	283	1	A45803	B-cell-restricted
473	96.5	6.2	288	2	S16385	macrophage colony-
474	96.5	6.2	978	2	A12216	hypothetical prote
475	96.5	6.2	249	2	S24284	single chain Fv an
476	96.5	6.2	499	1	S24607	Ig lambda chain -
477	96.5	6.2	1200	1	VGIHFS	platelet-derived g
478	96.5	6.2	1274	2	I52590	probable protein-t
479	96	6.2	1465	2	T50279	cardiac myosin-bin
480	96	6.2	282	2	D88976	165K protein, skel
481	96	6.2	466	2	I39428	hypothetical prote
482	96	6.2	572	2	I58411	killer cell inhibi
483	96	6.2	583	1	TVMSND	Ig Y heavy chain (
484	96	6.2	856	2	A59307	titin, muscle - ch
485	96	6.2	1147	1	A48594	MHC class I histoc
486	96	6.2	1666	2	A25757	Ig heavy chain - c
487	95.5	6.2	234	2	S41374	protein-tyrosine k
488	95.5	6.2	249	2	S33766	macrophage colony-
489	95.5	6.2	233	2	T43148	myosin-light-chain
490	95.5	6.2	216	2	S55050	skelemin - mouse
491	95.5	6.2	2132	1	S43529	Ig lambda chain -
492	95.5	6.2	2415	1	T17219	single chain Fv an
493	95.5	6.2	282	2	S25897	platelet-derived g
494	95	6.2	216	2	JC5897	aggrecan precursor
495	95	6.2	2132	1	B46529	aggrecan precursor
496	95	6.2	2124	1	A48721	proteoglycan core
497	95	6.2	941	1	I58142	aggrecan precursor
498	95	6.2	2124	1	A28452	Ig lambda chain -
499	95	6.2	234	2	A39086	Ig lambda chain (K
500	95	6.1	216	1	S03401	hypothetical prote
501	94.5	6.1	267	2	S25741	T-cell receptor be
502	94.5	6.1	335	2	PL0064	Ig lambda chain -
503	94.5	6.1	267	2	A53434	cell surface glyco
504	94.5	6.1	358	2	A28834	MHC class II histoc
505	94.5	6.1	1098	1	A53573	platelet-derived g
506	94.5	6.1	1449	1	AVMS67	protein-tyrosine k
507	94.5	6.1	975	1	S25746	E2 glycoprotein pr
508	94.5	6.1	1177	1	I54445	Ig heavy chain pre
509	94	6.1	344	1	F88639	Ig lambda chain -
510	94	6.1	236	2	TVMSKT	MHC H2-Qa-Mb1 - mo
511	94	6.1	433	1	T16594	protein C3-H4.3 [1
512	94.5	6.1	254	2	S21649	protein-tyrosine k
513	94	6.1	266	2	C42691	Ig lambda chain -
514	94	6.1	302	2	I56072	T-cell receptor be
515	93.5	6.1	154	2	C36464	fibroblast growth
516	93.5	6.1	326	2	WMVZ15	MHC class II HLA-D
517	93.5	6.1	302	2	E85843	MHC class II histo
518	93.5	6.1	281	2	HLHU1B	B15R protein precu
519	93.5	6.1	314	1	WMVZ16	fibroblast growth
520	93.5	6.1	314	1	WMVZVW	hemagglutinin prec
521	93	6.0	213	1	HNVZVW	hemagglutinin prec
522	93	6.0	2327	1	JQ1793	aggrecan - bovine
523	93	6.0	266	2	T42630	Ig lambda chain NI
524	93	6.0	213	2	JE0247	MHC class II histo
525	92.5	6.0	326	1	HLHUWB	Ig lambda chain V
526	92.5	6.0	345	2	T37450	vascular cell adhe
527	92.5	6.0	701	2	A46052	interleukin-1 beta
528	92.5	6.0	1327	2	T37243	hypothetical prote
529	92.5	6.0	217	2	T09402	immunoglobulin-lik
530	92	6.0	231	2	B25687	H-2 class II histo
531	92	6.0	274	2	S25753	Ig lambda chain -
532	92	6.0	310	1	S33440	T-cell receptor ga
533	92	6.0	568	2	HNVZRA	hemagglutinin prec
534	92	6.0	771	1	A34891	Ig heavy chain pre
535	92	6.0	229	2	D49423	semaphorin III p
536	92	5.9	229	2	AD1018	large repetitive p
537	91.5	5.9	2256	2	A20969	Ig kappa chain pre
538	91.5	5.9	235	2	S25058	Ig kappa chain - m
539	91.5	5.9	289	2	G00031	B7 protein - red-m
540	91.5	5.9	348	2	I68745	MHC class I lympho

541	91.5	5.9	358	2	B87063	conserved hypothet
542	91.5	5.9	391	2	S72717	Lepb170_F3_112 pr
543	91.5	5.9	568	2	A45804	Ig mu chain C regi
544	91.5	5.9	573	2	S12838	Ig mu chain precur
545	91.5	5.9	619	2	T15969	hypothetical prote
546	91.5	5.9	625	2	T16777	novel antigen rece
547	91.5	5.9	684	2	S60266	platelet-derived g
548	91.5	5.9	1048	2	T30815	Ig heavy chain V-5
549	91	5.9	117	2	E33989	T-cell receptor ga
550	91	5.9	202	2	S36293	class II histocomp
551	91	5.9	237	2	C27060	T-cell surface gly
552	91	5.9	240	2	A39016	gene HLA-DRB1 prot
553	91	5.9	266	2	I54287	hypothetical prote
554	91	5.9	266	2	A27618	class II histocomp
555	91	5.9	1649	2	C86822	hypothetical prote
556	91	5.9	2380	2	T29551	hypothetical prote
557	91	5.9	2468	2	A83412	cadherin-related t
558	91	5.9	5147	2	IJFFTM	Ig lambda chain -
559	91	5.9	162	2	I51668	tumor suppressor -
560	90.5	5.9	175	2	T01365	probable proline-r
561	90.5	5.9	178	2	S29594	Ig gamma chain (WM
562	90.5	5.9	232	2	S25742	Ig lambda chain -
563	90.5	5.9	233	2	JH0372	MHC class II histo
564	90.5	5.9	241	2	S32359	42K surface glycop
565	90.5	5.9	251	2	T15495	glial growth facto
566	90.5	5.9	266	2	A25324	hypothetical prote
567	90.5	5.9	266	2	I54448	class II histocomp
568	90.5	5.9	268	2	A56446	Ig heavy chain V r
569	90.5	5.9	315	1	HNVZVV	hemagglutinin prec
570	90.5	5.9	315	2	T37438	hemagglutinin - va
571	90.5	5.9	937	2	A45082	neurotrophic recep
572	90.5	5.9	1176	2	JN0583	myosin-light-chain
573	90.5	5.9	1449	2	S47423	E2 glycoprotein pr
574	90.5	5.9	116	2	A41527	protein-tyrosine k
575	90	5.9	231	2	B48218	neurexin III-alpha
576	90	5.9	323	2	S22556	Ig kappa-1 chain C
577	90	5.8	335	2	A48997	Ig lambda chain -
578	90	5.8	398	2	S09275	tumor surface anti
579	90	5.8	409	2	I49443	gene 2B4 protein -
580	90	5.8	531	2	T33019	hypothetical prote
581	90	5.8	661	2	B88109	protein T24E12.5 [
582	90	5.8	749	2	G82985	probable choline t
583	90	5.8	894	1	G01856	semaphorin V - hum
584	90	5.8	1471	2	A41527	protein-tyrosine k
585	89.5	5.8	104	2	F53275	neurexin III-alpha
586	89.5	5.8	231	2	S22556	Ig kappa-1 chain C
587	89.5	5.8	267	1	I72882	Fc gamma receptor
588	89.5	5.8	307	1	RWMSBC	T-cell receptor be
589	89.5	5.8	315	2	HNV24X	hemagglutinin prec
590	89.5	5.8	329	2	A40730	class I histocompa
591	89.5	5.8	422	2	S32357	glial growth facto
592	89.5	5.8	505	2	B46629	mucin 6, gastric (
593	89.5	5.8	531	2	S20900	titin - mouse (fra
594	89.5	5.8	599	2	T16774	hypothetical prote
595	89.5	5.8	692	2	G90284	hypothetical prote
596	89.5	5.8	767	1	JU0474	glucan 1,4-alpha-g
597	89.5	5.8	778	1	ALBYG	glucan 1,4-alpha-g
598	89.5	5.8	1014	2	T24412	hypothetical prote
599	89.5	5.8	1345	2	H90975	hypothetical prote
600	89.5	5.8	1526	2	T19473	hypothetical prote
601	89.5	5.8	3083	2	AH2493	hypothetical prote
602	89	5.8	182	2	A34647	pregnancy-specific
603	89	5.8	215	2	A57843	sodium channel bet
604	89	5.8	225	2	S37484	lymphocyte antigen
605	89	5.8	266	2	I54295	Ig kappa chain - m
606	89	5.8	309	2	S18894	T-cell receptor be
607	89	5.8	368	2	T24408	glial growth facto
608	89	5.8	454	2	A46532	Ig mu chain C regi
609	89	5.8	459	2	A46254	Ig mu chain C regi
610	89	5.8	459	2	C69377	CD4 precursor - ra
611	89	5.8	640	2	A43273	conserved hypothet
612	89	5.8	818	1	I49276	heregulin precurso
613	89	5.8	994	2	T14274	dipeptidyl aminope

614	89	5.8	1679	2	T30271	surface protein -
615	89	5.8	1691	2	D54689	protein-tyrosine-p
616	89	5.8	3381	2	T42389	versican precursor
617	89	5.8	13055	1	T16580	hypothetical prote
618	88.5	5.7	128	2	S24319	Ig lambda chain pr
619	88.5	5.7	182	2	A28508	T-cell surface gly
620	88.5	5.7	186	2	I61783	sodium channel bet
621	88.5	5.7	348	2	B39797	Ig alpha chain C r
622	88.5	5.7	348	2	S09273	MHC class II histo
623	88.5	5.7	356	2	A27797	class I histocompa
624	88.5	5.7	680	2	JC5895	killer cell inhibi
625	88.5	5.7	902	2	B90270	conserved hypothet
626	88.5	5.7	1578	2	AD1512	peptidoglycan boun
627	88	5.7	220	2	A49444	Ig gamma-1 heavy c
628	88	5.7	234	2	S14237	Ig kappa chain pre
629	88	5.7	241	2	D43273	heregulin precurso
630	88	5.7	270	2	A34636	Fc-gamma receptor
631	88	5.7	348	2	A56247	natural killer cel
632	88	5.7	376	2	T48950	cysteine proteinas
633	88	5.7	405	2	S33601	cell adhesion mole
634	88	5.7	451	2	T30603	perlecan homolog 2
635	88	5.7	462	2	I38404	neu differentiatio
636	88	5.7	645	2	C43273	heregulin, splice
637	88	5.7	694	2	B43273	heregulin precurso
638	88	5.7	974	1	A49714	protein-tyrosine k
639	88	5.7	1005	1	T18537	Ig heavy chain - c
640	87.5	5.7	104	1	K5RBV	Ig kappa chain C r
641	87.5	5.7	141	2	S31702	Ig heavy chain V r
642	87.5	5.7	237	2	H28043	MHC class II histo
643	87.5	5.7	264	2	A60497	H-2 class II histo
644	87.5	5.7	307	2	S55596	hypothetical prote
645	87.5	5.7	562	2	G02426	interleukin-1 rece
646	87.5	5.7	694	2	C83826	penicillin-binding
647	87.5	5.7	1999	2	AB2018	hypothetical prote
648	87.5	5.7	2383	2	D64962	probable membrane
649	87.5	5.7	2409	2	A60979	versican precursor
650	87.5	5.7	4936	2	AH2515	probable invasin 2
651	87	5.7	137	2	C45893	Ig lambda chain C
652	87	5.7	142	2	S10004	hypothetical prote
653	87	5.7	151	2	EVRTR2	T-cell receptor al
654	87	5.7	164	2	T19795	hypothetical prote
655	87	5.7	166	2	JC7761	dendritic cell-der
656	87	5.7	216	2	G28043	MHC class II histo
657	87	5.6	230	2	I67482	MHC class I heavy
658	87	5.6	357	2	A42193	neu differentiatio
659	87	5.6	510	2	A56210	Ig lambda chain (B
660	87	5.6	570	2	PC4054	cardiac C-protein
661	87	5.6	103	2	A57535	interleukin-1 rece
662	86.5	5.6	135	2	B85822	hypothetical prote
663	86.5	5.6	142	2	B26167	Ig lambda chain C
664	86.5	5.6	151	2	S10004	hypothetical prote
665	86.5	5.6	166	2	PL0011	Ig heavy chain pre
666	86.5	5.6	166	2	PL0011	Ig lambda chain -
667	86.5	5.6	216	2	G28043	Ig lambda chain -
668	86.5	5.6	240	2	S25758	Ig kappa chain pre
669	86.5	5.6	266	2	B27618	MHC class II histo
670	86.5	5.6	266	2	A45856	Ig gamma-1 chain C
671	86.5	5.6	330	1	GHHU	Ig alpha chain C r
672	86.5	5.6	343	2	S09272	MHC class II histo
673	86.5	5.6	487	2	S65133	butyrophilin - mou
674	86.5	5.6	511	1	VGBE1K	glycoprotein C - h
675	86.5	5.6	580	2	A46538	Ig heavy chain, se
676	86.5	5.6	636	2	I61718	Ig heavy chain V r
677	86.5	5.6	639	2	I61719	neu differentiatio
678	86.5	5.6	662	2	I61722	neu differentiatio
679	86.5	5.6	719	2	F82831	polynucleotide pho
680	86.5	5.6	751	2	I48748	semaphorin E - mou
681	86.5	5.6	1832	2	T31113	mucin-like glycopr
682	86	5.6	125	2	S68170	semaphorin E - mou
683	86	5.6	210	2	S25657	T-cell surface gly
684	86	5.6	335	2	S58892	signaling lymphocy
685	86	5.6	339	2	JC7509	glycoprotein VI-1
686	86	5.6	347	2	S41638	T-cell surface gly

Seq	%		Len		Accession	Description
687	86	5.6	362	2	A45845	MHC class I histoc
688	86	5.6	367	2	T12790	N-acetylmuramoyl-L-
689	86	5.6	416	2	A54017	colon carcinoma-as
690	86	5.6	545	2	JU03411	intercellular adhe
691	86	5.6	975	2	T30816	macrophage colony-
692	86	5.6	983	2	A45583	receptor tyrosine
693	85.5	5.6	178	2	PT0219	Ig kappa chain V-C
694	85.5	5.6	221	2	S49220	Ig gamma-1 chain -
695	85.5	5.6	266	2	A28031	MHC class II chain -
696	85.5	5.5	266	2	I54509	MHC class II histo
697	85.5	5.5	277	2	I52825	MHC class II HLA-D
698	85.5	5.5	282	2	S50031	gene MAC25 protein
699	85.5	5.5	303	2	JE0128	prostacyclin-stimu
700	85.5	5.5	400	2	A40807	membrane glycoprot
701	85.5	5.5	403	2	T34363	hypothetical prote
702	85.5	5.5	473	1	MHHUM	argininosuccinate
703	85.5	5.5	772	2	A49069	Ig mu chain C regi
704	85.5	5.5	277	2	A33998	collapsin - chicke
705	85.5	5.5	1181	2	I51715	integrin alpha-2 c
706	85.5	5.5	1715	2	C39797	Bombyx mori recept
707	85	5.5	269	2	S22552	Ig gamma-4 chain C
708	85	5.5	265	2	H36005	MHC class II histo
709	85	5.5	197	2	S29593	MHC class II beta-
710	85	5.5	121	2	T13797	Ig kappa chain V r
711	85	5.5	117	2	D97316	Ig heavy chain V r
712	85	5.5	1477	2	B95075	tumor supressor pr
713	85	5.5	1939	2	T22945	hypothetical prote
714	85	5.5	2233	2	PL0232	probable S-layer p
715	85	5.5	3191	2	A24402	beta-galactosidase
716	85	5.5	112	2	JL0029	hypothetical prote
717	85	5.5	132	2	D72174	Ig heavy chain V r
718	84.5	5.5	225	2	I60125	T-cell receptor al
719	84.5	5.5	355	2	I51174	Ig kappa chain pre
720	84.5	5.5	375	2	A39371	D9R protein - vari
721	84.5	5.5	381	2	G86466	PDGF receptor beta
722	84.5	5.5	398	1	HVRKCS	Ig heavy chain - R
723	84.5	5.5	438	2	A46533	Ig V-region-like B
724	84.5	5.5	448	2	S03961	Ig mu chain C regi
725	84.5	5.5	457	1	HVRKCO	Ig heavy chain C r
726	84.5	5.5	461	2	A37821	Ig mu chain C regi
727	84.5	5.5	526	2	AC0424	butyrophilin - bov
728	84.5	5.5	705	2	T21888	polyribonucleotide
729	84.5	5.5	1797	2	E97944	hypothetical prote
730	84.5	5.5	1805	2	G47624	beta-galactosidase
731	84.5	5.5	2228	2	I46633	Ig heavy chain V-v
732	84	5.4	98	2	A41675	rearranged T-cell
733	84	5.4	145	2	G90290	telokin - rabbit
734	84	5.4	155	2	A53273	hypothetical prote
735	84	5.4	220	2	S25738	MHC class II histo
736	84	5.4	226	2	A39956	MHC class II histo
737	84	5.4	231	2	I54294	Ig lambda chain pr
738	84	5.4	234	2	S25663	MHC HLA-DR-beta su
739	84	5.4	237	2	S09266	T-cell surface gly
740	84	5.4	242	2	I61867	hypothetical prote
741	84	5.4	247	1	MHHU	myelin P0 protein
742	84	5.4	321	2	S31459	hypothetical prote
743	84	5.4	352	2	D86298	Ig alpha chain C r
744	84	5.4	359	2	A45769	MHC class I protei
745	84	5.4	452	2	I59372	Ig mu chain C regi
746	84	5.4	472	2	H82543	Ig gamma-1 chain -
747	84	5.4	498	2	JC7294	hypothetical prote
748	84	5.4	602	2	C97033	acetylcholine rece
749	84	5.4	794	2	E89066	cadherin 12 - huma
750	84	5.4	893	2	T33247	DNA gyrase subunit
751	84	5.4	1054	2	I59092	alphaP integrin -
752	84	5.4	1227	2	G83458	uncharacterized pr
753	84	5.4	2109	2	I54551	protein H05009.1 [
754	84	5.4	2109	2	A30521	HLA-DR beta-chain
755	83.5	5.4	246	2		sulfate-binding pr
756	83.5	5.4	332	2		histocompatibility
757	83.5	5.4	354	2		myeloid cell surfa
758	83.5	5.4	364	2		
759	83.5	5.4				

Seq	%		Len		Accession	Description
760	83.5	5.4	476	2	T25736	hypothetical proce
761	83.5	5.4	627	2	S14683	Ig mu chain precur
762	83.5	5.4	975	2	I48974	receptor-protein t
763	83.5	5.4	1495	2	T31434	tenascin precursor
764	83.5	5.4	1810	2	A32230	densin-180 - rat
765	83.5	5.4	3033	1	JQ1303	genome polyprotein
766	83.5	5.4	119	2	PS0091	Ig heavy chain V r
767	83	5.4	149	2	S30752	class II histocomp
768	83	5.4	200	2	D32526	MHC class II beta
769	83	5.4	247	2	I69002	histocompatibility
770	83	5.4	354	2	S35695	hypothetical prote
771	83	5.4	358	2	B75197	glia-derived nexin
772	83	5.4	398	2	A37274	neurexin III beta
773	83	5.4	426	2	B53580	tyrosine kinase C
774	83	5.4	525	1	A58674	cytotactin - chick
775	83	5.4	537	2	A46611	tyrosine kinase Mp
776	83	5.4	247	2	G85021	neurotrophin-3 rec
777	83	5.4	803	2	S35695	myosin-binding pro
778	83	5.4	852	2	I51259	protoporphyrinogen
779	83	5.4	933	2	A31930	neurotrophin-3 rec
780	83	5.4	977	2	S49004	tyrosine kinase C
781	83	5.4	1036	2	T30311	MHC class II histoc
782	82.5	5.4	1055	2	PH0978	MHC class II DR-be
783	82.5	5.4	237	2	B30598	MHC class II histo
784	82.5	5.4	248	1	F27060	Ig gamma-2 chain C
785	82.5	5.3	569	2	T00756	MHC class I histoc
786	82.5	5.3	609	2	A36187	CD44R5 - human
787	82.5	5.3	719	2	G87496	proteoglycan link
788	82.5	5.3	775	2	S63629	hypothetical prote
789	82.5	5.3	812	2	S63626	T-cell surface gly
790	82.5	5.3	826	2	T27007	hypothetical prote
791	82.5	5.3	894	2	T52569	interleukin-1 rece
792	82.5	5.3	896	2	B55363	peptidase, M23/M37
793	82.5	5.3	914	2	A55363	homeotic protein A
794	82.5	5.3	1035	2	C69284	homeotic protein A
795	82.5	5.3	1200	2	G86342	desmocollin, type
796	82.5	5.3	1530	1	T17404	desmocollin, type
797	82.5	5.3	362	1	AH1396	equamosa-promoter
798	82.5	5.3	395	2	B34509	surface layer prot
799	82.5	5.3	408	1	S24683	hyalin - sea urchi
800	82.5	5.3	419	2	S40342	peptidoglycan anch
801	82.5	5.3	432	1	RWMQT4	Ig light chain C r
802	82.5	5.3	436	2	T00756	Ig heavy chain V6
803	82.5	5.3	569	2	A36187	Ig kappa chain - h
804	82.5	5.3	609	2	S63626	Ig lambda chain - B
805	82.5	5.3	719	2	S63629	Ig kappa chain V-
806	82.5	5.3	826	2	T27007	Ig mu chain C regi
807	82	5.3	102	2	B34509	MHC class II beta-
808	82	5.3	119	2	S24683	MHC class II beta-
809	82	5.3	135	2	S02083	class II histocomp
810	82	5.3	146	2	S33161	MHC class I protei
811	82	5.3	230	2	S33161	streptogramin lyas
812	82	5.3	249	2	I50464	MHC class II histoc
813	82	5.3	260	2	I51542	intercellular adhe
814	82	5.3	269	2	I51539	intercellular adhe
815	82	5.3	296	2	S01441	protoporphyrinogen
816	82	5.3	350	2	I50015	intercellular adhe
817	82	5.3	352	2	S76078	Ig mu chain C regi
818	82	5.3	367	1	MHCH	MHC class II protei
819	82	5.3	531	2	S06016	MHC class II beta-
820	82	5.3	537	2	I49769	MHC class II beta-
821	82	5.3	537	2	A45815	myosin-binding pro
822	82	5.3	545	2	T02005	connectin 1 - chic
823	82	5.3	743	2	T42557	hypothetical prote
824	82	5.3	764	2	S50878	tegument protein 1
825	82	5.3	811	2	PN0689	hypothetical prote
826	82	5.3	1132	2	A35089	Ig kappa chain V-
827	82	5.3	3507	2	T34513	Ig lambda chain - B
828	81.5	5.3	111	2	PH1573	T-cell surface gly
829	81.5	5.3	121	2	A30551	hypothetical prote
830	81.5	5.3	139	2	E27639	T-cell receptor be
831	81.5	5.3	144	2	B40098	Ig heavy chain V r
832	81.5	5.3	212	2	S70431	T-cell receptor ga

No.	Score		Len	N	Code	Description
833	81.5	5.3	270	2	I51543	MHC class II beta-
834	81.5	5.3	285	2	S35903	Fc gamma (IgG) rec
835	81.5	5.3	305	2	S07115	class I histocompa
836	81.5	5.3	308	2	I36956	MHC ChiA chain - c
837	81.5	5.3	354	2	I80170	class I histocompa
838	81.5	5.3	354	2	S46877	B2OR protein - var
839	81.5	5.3	354	2	T28616	hypothetical prote
840	81.5	5.3	354	2	S24438	class I histocompa
841	81.5	5.3	354	2	S24440	class I histocompa
842	81.5	5.3	358	2	S03538	class I histocompa
843	81.5	5.3	359	1	HLHUB4	MHC class I histoc
844	81.5	5.3	362	2	HLHU40	MHC HLA-B8 chain
845	81.5	5.3	362	1	HLHUB7	MHC HLA-B14 chain
846	81.5	5.3	362	2	I36962	MHC class I protei
847	81.5	5.3	362	2	I84488	lymphocyte antigen
848	81.5	5.3	362	2	I54505	MHC class I histoc
849	81.5	5.3	362	2	I54314	MHC HLA-B39N - hum
850	81.5	5.3	362	2	S60601	HLA-BPOT (classI)
851	81.5	5.3	362	2	I59645	MHC class I histoc
852	81.5	5.3	362	2	I68850	HLA-B-6701 - human
853	81.5	5.3	362	2	I61903	MHC class I histoc
854	81.5	5.3	362	2	I61859	MHC class I histoc
855	81.5	5.3	362	2	I59651	lymphocyte antigen
856	81.5	5.3	365	2	I56053	class I histocompa
857	81.5	5.3	492	2	A97429	figK protein prote
858	81.5	5.3	492	2	A82647	hook associated pr
859	81.5	5.3	578	1	T41715	nerve growth facto
860	81.5	5.3	790	1	TVHUTT	hypothetical prote
861	81.5	5.3	842	2	T04555	MHC class I histoc
862	81.5	5.3	896	2	I45858	desmocollin - bovi
863	81.5	5.3	953	2	C89824	hypothetical prote
864	81.5	5.3	978	1	A49814	protein-tyrosine k
865	81.5	5.3	1389	2	T47796	ABC transporter-li
866	81.5	5.3	1559	1	S64757	probable membrane
867	81	5.2	1159	2	A24672	Ig heavy chain pre
868	81	5.2	127	2	S70444	Ig lambda chain pr
869	81	5.2	143	2	PT0174	Ig heavy chain pre
870	81	5.2	144	2	I46642	rearranged T-cell
871	81	5.2	196	2	T19794	hypothetical prote
872	81	5.2	210	2	E46482	T-cell surface gly
873	81	5.2	214	2	PC4156	Ig lambda chain V
874	81	5.2	217	2	JE0246	Ig lambda chain NI
875	81	5.2	221	2	C46482	T-cell surface gly
876	81	5.2	237	1	E28043	brevican precursor
877	81	5.2	246	2	T01073	MHC class II histo
878	81	5.2	247	2	I50093	MHC class II beta
879	81	5.2	252	2	A46505	SLA-DRAd (MHC Clas
880	81	5.2	266	2	A29310	MHC class II histo
881	81	5.2	321	2	A71510	hypothetical prote
882	81	5.2	351	1	SAVZVV	surface antigen pr
883	81	5.2	378	2	I46268	brevican precursor
884	81	5.2	426	1	I36948	Ig epsilon-chain -
885	81	5.2	454	1	MHHY	Ig mu chain C regi
886	81	5.2	631	1	I52257	epsialin - mouse
887	81	5.2	666	2	JE0201	protein-tyrosine k
888	81	5.2	666	1	T34288	semaphorin III - m
889	81	5.2	748	2	I48744	semaphorin A - mou
890	81	5.2	942	2	T20287	hypothetical prote
891	81	5.2	943	2	B45082	neurotrophic recep
892	81	5.2	983	2	A38224	protein-tyrosine k
893	81	5.2	1146	2	S46837	hypothetical prote
894	81	5.2	1747	2	A45974	collagen alpha 1(X
895	81	5.2	1827	2	T34288	hypothetical prote
896	81	5.2	1902	2	S06997	lactocepin (EC 3.4
897	81	5.2	1902	2	B45764	lactocepin (EC 3.4
898	81	5.2	3343	2	T42207	breast cancer susc
899	80.5	5.2	105	2	B30554	Ig lambda chain C
900	80.5	5.2	139	2	F27639	T-cell receptor ga
901	80.5	5.2	215	2	JE0243	Ig kappa chain NIG
902	80.5	5.2	251	2	I38053	myelin protein zer
903	80.5	5.2	264	2	S10989	FC gamma 1 recepto
904	80.5	5.2	264	2	I46020	class II histocomp
905	80.5	5.2	290	2	AG2216	hypothetical prote
906	80.5	5.2	338	2	I56116	MHC HLA-B27-HS - h
907	80.5	5.2	350	2	I68747	MHC class I lympho
908	80.5	5.2	354	2	I80165	class I histocompa
909	80.5	5.2	355	2	T24149	MHC HLA-B8 chain -
910	80.5	5.2	361	2	I54418	class I histoc
911	80.5	5.2	362	1	HLHUB2	MHC class I histoc
912	80.5	5.2	362	2	I37492	MHC class I histoc
913	80.5	5.2	362	2	S52486	HLA-B alpha-chain
914	80.5	5.2	362	2	I56149	lymphocyte antigen
915	80.5	5.2	362	2	A45850	MHC HLA-Bw41 chain
916	80.5	5.2	362	2	I61906	MHC HLA-B41 chain
917	80.5	5.2	362	2	I59655	MHC class I histoc
918	80.5	5.2	362	2	I84431	lymphocyte antigen
919	80.5	5.2	362	2	I54442	MHC class I histoc
920	80.5	5.2	362	2	I61905	MHC class I histoc
921	80.5	5.2	362	2	I61865	MHC HLA-Bw42, HLA-
922	80.5	5.2	364	2	D35997	MHC class I histoc
923	80.5	5.2	476	2	T27618	hypothetical prote
924	80.5	5.2	605	2	S67815	protein-tyrosine k
925	80.5	5.2	605	2	S49745	probable membrane
926	80.5	5.2	661	2	E71427	hypothetical prote
927	80.5	5.2	706	2	H81943	probable polyribon
928	80.5	5.2	707	2	C81161	polyribonucleotide
929	80.5	5.2	834	2	T42702	hypothetical prote
930	80.5	5.2	936	2	S64384	probable membrane
931	80.5	5.2	936	1	PHI286	probable membrane
932	80.5	5.2	1134	2	JN0711	hypothetical prote
933	80.5	5.2	2123	2	P86348	protein-tyrosine k
934	80.5	5.2	2626	2	T31099	hypothetical prote
935	80.5	5.2	118	2	S18556	Ig mu chain C regi
936	80	5.2	133	1	PHI286	myosin-RhoGAP prot
937	80	5.2	144	2	S25740	protein-tyrosine k
938	80	5.2	190	2	A86344	protein T22III.8 [
939	80	5.2	233	2	AE0472	probable fimbrial
940	80	5.2	243	2	S29980	class II histocomp
941	80	5.2	245	2	D46482	T-cell surface gly
942	80	5.2	246	1	HLHU5D	MHC class II histo
943	80	5.2	266	2	D39797	MHC class II histo
944	80	5.2	333	2	T27883	hypothetical prote
945	80	5.2	344	1	RWRTC2	T-cell surface gly
946	80	5.2	353	2	SAV2VC	surface antigen pr
947	80	5.2	353	1	T40476	hypothetical serin
948	80	5.2	393	1	HVRKC1	Ig mu chain C regi
949	80	5.2	432	1	JC7576	hypothetical prote
950	80	5.2	458	2	T19785	transcription fact
951	80	5.2	484	2	C88264	hypothetical prote
952	80	5.2	488	2	I44330	MHC class II histo
953	80	5.2	536	2	T37544	hypothetical prote
954	80	5.2	576	2	T40476	hypothetical prote
955	80	5.2	615	2	JC7576	hypothetical prote
956	80	5.2	654	2	A96315	hypothetical prote
957	80	5.2	708	2	E86774	hypothetical prote
958	80	5.2	749	1	AG2315	Ig mu chain C regi
959	80	5.2	888	2	S23065	ufo protein - mous
960	80	5.2	942	2	S23251	protein-tyrosine k
961	80	5.2	1053	2	I55534	hypothetical prote
962	80	5.2	1081	2	S51899	probable protein k
963	80	5.2	1185	2	T46428	hypothetical prote
964	80	5.2	1537	2	S53465	flocculation prote
965	80	5.1	1848	2	A44140	cellulose-binding
966	79.5	5.1	105	1	LIPG	Ig lambda chain C
967	79.5	5.1	119	2	S18555	Ig heavy chain V r
968	79.5	5.1	119	2	C33876	carcinoembryonic a
969	79.5	5.1	120	2	A32072	Ig heavy chain pre
970	79.5	5.1	131	2	T20334	hypothetical prote
971	79.5	5.2	136	2	B45893	T-cell receptor al
972	79.5	5.1	136	2	A26471	Ig kappa chain pre
973	79.5	5.1	138	2	T05849	hypothetical prote
974	79.5	5.1	156	2	I55849	MHC class II E-bet
975	79.5	5.1	245	2	I55951	MHC class II prote
976	79.5	5.1	253	2	T49416	hypothetical prote
977	79.5	5.1	257	2	S29981	MHC class II beta-
978	79.5	5.1	267	2	A35902	Fc gamma (IgG) rec

No.			Length	N	Accession	Description
979	79.5	5.1	284	2	S09769	hypothetical prote
980	79.5	5.1	291	2	A70475	H+-transporting tw
981	79.5	5.1	304	2	S65198	hypothetical prote
982	79.5	5.1	325	2	T36434	threonine ammonia-
983	79.5	5.1	325	2	T03010	probable replicati
984	79.5	5.1	327	2	AF0618	conserved hypothet
985	79.5	5.1	335	2	A87135	hypothetical membr
986	79.5	5.1	354	2	VGBEF2	probable membrane
987	79.5	5.1	354	2	S24433	class I histocompa
988	79.5	5.1	354	2	S24436	class I histocompa
989	79.5	5.1	354	2	S24437	class I histocompa
990	79.5	5.1	360	2	S09271	Ig alpha chain C r
991	79.5	5.1	361	2	JH0417	cell adhesion mole
992	79.5	5.1	362	2	S56130	HLA-B*5401 - human
993	79.5	5.1	362	2	I84486	transmembrane glyc
994	79.5	5.1	362	2	I62042	MHC HLA-B cell sur
995	79.5	5.1	362	2	I37120	MHC class I histoc
996	79.5	5.1	362	2	B30345	MHC class I histoc
997	79.5	5.1	362	2	A45834	MHC class I histoc
998	79.5	5.1	362	2	I61907	MHC class I histoc
999	79.5	5.1	362	2	I37515	MHC class I histoc
1000	79.5	5.1	362	2	C35997	MHC class I histoc
1001	79.5	5.1	362	2	I81233	lymphocyte antigen
1002	79.5	5.1	362	2	I72754	HLA-B*5602 - human
1003	79.5	5.1	362	2	G01230	MHC class I histoc
1004	79.5	5.1	362	2	I37522	MHC class I histoc
1005	79.5	5.1	362	2	I59633	MHC HLA-B transmem
1006	79.5	5.1	362	2	I61904	MHC class I histoc
1007	79.5	5.1	362	2	I72753	HLA-B*5502 - human
1008	79.5	5.1	362	2	I59654	major histocompati
1009	79.5	5.1	362	2	I72752	HLA-B*5601 - human
1010	79.5	5.1	362	2	I62045	gene HLA B-1517 pr
1011	79.5	5.1	362	2	I61863	MHC HLA-Bw46 - hum
1012	79.5	5.1	362	2	I37519	MHC class I histoc
1013	79.5	5.1	362	2	I37519	MHC class I histoc
1014	79.5	5.1	362	2	I54457	HLA-B*5501 - lympho
1015	79.5	5.1	362	2	I72752	MHC class I histoc
1016	79.5	5.1	362	2	I56133	MHC class I protei
1017	79.5	5.1	362	2	I54298	lymphocyte antigen
1018	79.5	5.1	362	2	I84490	gene HLA-B protein
1019	79.5	5.1	362	2	I61865	MHC class I histoc
1020	79.5	5.1	362	2	I62043	MHC class I histoc
1021	79.5	5.1	362	2	I37520	MHC class I histoc
1022	79.5	5.1	362	2	I62041	MHC class I histoc
1023	79.5	5.1	362	2	I62044	MHC class I histoc
1024	79.5	5.1	362	2	I61860	MHC HLA-B18 chain
1025	79.5	5.1	362	2	S16789	class I histocompa
1026	79.5	5.1	362	2	S24435	class I histocompa
1027	79.5	5.1	362	2	S24434	hypothetical prote
1028	79.5	5.1	363	2	H97455	UDP-N-acetylglucos
1029	79.5	5.1	363	2	F82020	C4-dicarboxylate t
1030	79.5	5.1	428	2	S47749	uptake of C4-dicar
1031	79.5	5.1	428	2	A86026	uptake of C4-dicar
1032	79.5	5.1	428	2	H91179	serine-rich protei
1033	79.5	5.1	534	2	T39903	hypothetical prote
1034	79.5	5.1	547	2	S61032	killer cell inhibi
1035	79.5	5.1	635	2	JC5896	protein P20B24.6 [
1036	79.5	5.1	715	2	G86239	S-receptor kinase
1037	79.5	5.1	824	1	S50767	macrophage colony-
1038	79.5	5.1	972	2	TVHUMD	cartilage intermed
1039	79.5	5.1	1184	2	T09484	hypothetical prote
1040	79.5	5.1	2167	2	T34395	probable invasin Y
1041	79.5	5.1	3013	2	AB0480	large repetitive p
1042	79.5	5.1	3624	2	AD0835	carcinoembryonic a
1043	79	5.1	85	2	S08109	Ig heavy chain V r
1044	79	5.1	98	2	S26914	T-cell receptor be
1045	79	5.1	111	2	E27552	T-cell receptor be
1046	79	5.1	140	2	S54248	Ig heavy chain V r
1047	79	5.1	140	2	PH1482	Ig mu heavy chain
1048	79	5.1	154	2	S23044	T-cell receptor ga
1049	79	5.1	244	2	S29982	Ig heavy chain V r
1050	79	5.1	252	2	S69786	class II histocomp
1051	79	5.1	253	2	S15684	prgK protein - Sal
1052	79	5.1	267	2	I56110	Fc-gamma RIIB-alp
1053	79	5.1	333	2	PS0018	Ig gamma-2b chain
1054	79	5.1	351	1	SAVZWR	surface antigen pr
1055	79	5.1	355	2	B40730	class I histocompa
1056	79	5.1	376	2	E85435	class I histocompa
1057	79	5.1	421	2	T10190	cysteine proteinas
1058	79	5.1	430	2	H72604	L-ascorbate peroxi
1059	79	5.1	479	1	VGBEF2	hypothetical prote
1060	79	5.1	492	2	AH1030	glycoprotein F - h
1061	79	5.1	479	2	F83421	probable exported
1062	79	5.1	430	2	T47542	glutaminyl-tRNA sy
1063	79	5.1	623	2	T38470	Spot 3 protein and
1064	79	5.1	556	2	T09484	probable calcium-t
1065	79	5.1	1609	2	S36859	probable membrane
1066	79	5.1	1854	2	S35345	cipA protein - Clo
1067	79	5.1	1902	1	B44858	lactocepin (EC 3.4
1068	78.5	5.1	109	2	PL0233	Ig heavy chain V r
1069	78.5	5.1	114	2	S22554	Ig heavy chain V r
1070	78.5	5.1	123	2	PH1403	Ig heavy chain V6
1071	78.5	5.1	125	2	S24703	Ig heavy chain V r
1072	78.5	5.1	136	2	S04576	T-cell receptor de
1073	78.5	5.1	139	2	S36325	Ig heavy chain pre
1074	78.5	5.1	182	1	C37410	MHC class II histo
1075	78.5	5.1	220	2	I67726	H-2 class II histo
1076	78.5	5.1	236	2	I68710	HLA class II histo
1077	78.5	5.1	239	2	I46860	MHC R1A - rabbit (
1078	78.5	5.1	248	1	B04886	probable VAMP-asso
1079	78.5	5.1	264	2	JH0252	myelin P0 protein
1080	78.5	5.1	265	1	I48422	MHC class II histo
1081	78.5	5.1	266	2	S24703	carcinoembryonic a
1082	78.5	5.1	326	2	S69335	cell surface glyco
1083	78.5	5.1	359	1	S04576	transcription fact
1084	78.5	5.1	354	2	S36325	myristoylated alan
1085	78.5	5.1	354	2	HLHU12	class I histocompa
1086	78.5	5.1	354	2	I68724	class I histocompa
1087	78.5	5.1	354	2	A45452	class I histocompa
1088	78.5	5.1	362	2	S08341	MHC class I histoc
1089	78.5	5.1	399	2	A30901	lymphocyte adhesio
1090	78.5	5.1	432	2	S27879	secretory protein
1091	78.5	5.1	450	1	I48343	interleukin-11 rec
1092	78.5	5.1	453	2	MHDG	Ig mu chain C regi
1093	78.5	5.1	477	2	S37768	Ig mu chain C regi
1094	78.5	5.1	479	1	S53362	mucin 5AC (clone J
1095	78.5	5.1	518	2	S15031	paired box transcr
1096	78.5	5.1	556	2	T49778	hypothetical prote
1097	78.5	5.1	576	2	T16143	hypothetical prote
1098	78.5	5.1	595	2	A32604	interleukin-1 rece
1099	78.5	5.1	712	2	A35847	Fos-related antige
1100	78.5	5.1	719	2	S44237	hypothetical prote
1101	78.5	5.1	740	2	G95153	trypomastigote sur
1102	78.5	5.1	1378	1	I48751	neuraminidase, pro
1103	78.5	5.1	1539	2	S65775	protein-tyrosine k
1104	78.5	5.1	1821	2	AG2335	homeotic protein H
1105	78.5	5.1	1965	1	S75200	hypothetical prote
1106	78	5.1	118	2	S25174	fat protein - Syne
1107	78	5.1	127	2	S04577	Ig heavy chain V r
1108	78	5.1	133	2	PH1288	Ig kappa chain pre
1109	78	5.1	137	2	S54234	Ig heavy chain pre
1110	78	5.1	233	1	JU0284	Ig mu heavy chain
1111	78	5.1	239	2	I55966	Fc gamma (IgG) rec
1112	78	5.1	252	2	I71904	HLA DR-beta-III -
1113	78	5.1	253	2	JC2388	HLA DR-beta-III -
1114	78	5.1	254	2	A71624	class II histocomp
1115	78	5.1	299	1	AHRB	probable integral
1116	78	5.1	338	2	S09276	Ig alpha chain C r
1117	78	5.1	400	1	A29822	Ig alpha chain C r
1118	78	5.1	402	2	S20002	leukosialin precur
1119	78	5.1	433	2	S31436	Ig heavy chain, se
1120	78	5.1	433	2	JL0144	Ig upsilon chain,
1121	78	5.1	440	2	JL0147	interleukin-6 rece
1122	78	5.1	460	2	JL0145	interleukin-6 rece
1123	78	5.1	550	2	AI1163	flagellar basal-bo
1124	78	5.1	624	2	T00044	vacuolar sorting r

No.			Len	N	Code	Description
1125	78	5.1	678	2	T39151	translation initia
1126	78	5.1	744	2	A43353	acites sialoglyco
1127	78	5.1	857	2	S44883	ZC262.3 protein -
1128	78	5.1	875	2	H90371	proteinase [import
1129	78	5.1	902	2	T47966	hypothetical prote
1130	78	5.1	912	2	D72644	hypothetical prote
1131	78	5.1	1081	2	T31094	surface antigen Bs
1132	78	5.1	1123	2	C96622	probable ATPase P2
1133	78	5.1	1188	2	JC4889	phosphatidylinosit
1134	78	5.1	1219	2	T14578	nucleoporin Nup153
1135	78	5.1	2287	2	T21312	hypothetical prote
1136	78	5.1	103	1	K5RB	Ig kappa-B5 chain
1137	77.5	5.0	119	2	S45714	Ig heavy chain v r
1138	77.5	5.0	134	2	A45893	T-cell receptor al
1139	77.5	5.0	149	2	B40463	integrin alpha-6 c
1140	77.5	5.0	150	2	PN0444	Ig heavy chain v r
1141	77.5	5.0	215	2	S61337	proteasome endopep
1142	77.5	5.0	219	1	A29128	myelin P0 protein
1143	77.5	5.0	232	1	HLMSE2	H-2 class II histo
1144	77.5	5.0	237	2	A21200	H-2 class II histo
1145	77.5	5.0	241	2	H96691	hypothetical prote
1146	77.5	5.0	249	2	S69340	Ig heavy chain VHI
1147	77.5	5.0	250	2	A28564	lymphocyte functio
1148	77.5	5.0	250	2	S19518	hypothetical prote
1149	77.5	5.0	264	2	T26976	MHC class II histo
1150	77.5	5.0	266	2	B28031	hypothetical prote
1151	77.5	5.0	300	2	T34071	hypothetical prote
1152	77.5	5.0	309	2	T15747	hypothetical prote
1153	77.5	5.0	348	2	S09270	Ig alpha chain C r
1154	77.5	5.0	350	2	I54308	MHC HLA B71 - huma
1155	77.5	5.0	382	2	T46519	probable glycosyl
1156	77.5	5.0	391	1	MHHUBT	Ig mu heavy chain
1157	77.5	5.0	430	2	T28143	tapasin 1 homolog,
1158	77.5	5.0	462	2	AH1184	wall associated pr
1159	77.5	5.0	465	2	A4498	radial spoke prote
1160	77.5	5.0	477	2	H75026	oligopeptide abc t
1161	77.5	5.0	498	2	S11246	LAG-3 protein prec
1162	77.5	5.0	555	2	JQ1526	interleukin-1 rece
1163	77.5	5.0	590	2	B86440	probable protein k
1164	77.5	5.0	634	2	C96541	10-formyltetrahydr
1165	77.5	5.0	679	2	S06000	penicillin-binding
1166	77.5	5.0	966	2	H99717	hypothetical prote
1167	77.5	5.0	987	2	B70808	probable PPE prote
1168	77.5	5.0	1027	2	D85757	probable efflux pu
1169	77.5	5.0	1027	2	H90861	probable multidrug
1170	77.5	5.0	1073	2	B36429	integrin alpha-6 c
1171	77.5	5.0	1353	2	T00249	ichl protein - ink
1172	77.5	5.0	1441	2	A86685	prophage pil prote
1173	77.5	5.0	1452	1	S17669	protein-tyrosine-p
1174	77.5	5.0	1452	1	S17670	protein-tyrosine-p
1175	77.5	5.0	2044	2	ABI180	probable peptidogl
1176	77.5	5.0	4302	2	A38971	polycystic kidney
1177	77.5	5.0	118	2	B32536	T-cell receptor al
1178	77.5	5.0	130	2	S04542	T-cell receptor be
1179	77.5	5.0	134	2	PC1214	Ig kappa chain pre
1180	77.5	5.0	135	2	PH1492	Ig heavy chain v r
1181	77.5	5.0	137	2	PH1227	Ig heavy chain v r
1182	77.5	5.0	140	1	HVMSG7	Ig heavy chain pre
1183	77.5	5.0	140	2	A36194	Ig heavy chain v r
1184	77.5	5.0	144	2	PH1483	Ig heavy chain pre
1185	77.5	5.0	144	2	PH1284	Ig heavy chain pre
1186	77.5	5.0	216	2	S69130	Ig lambda chain (D
1187	77.5	5.0	219	2	PC4203	Ig kappa chain (mo
1188	77.5	5.0	229	2	A48381	MHC class II histo
1189	77.5	5.0	259	2	A98049	conserved hypothet
1190	77.5	5.0	259	2	F95181	conserved hypothet
1191	77.5	5.0	350	2	I46608	MHC PD6-glycoprote
1192	77.5	5.0	352	2	I51541	MHC class I antige
1193	77.5	5.0	353	2	B52250	class I histocompa
1194	77.5	5.0	355	2	I51309	major histocompati
1195	77	5.0	355	2	I80169	class I histocompa
1196	77	5.0	357	2	S09269	Ig alpha chain C r
1197	77	5.0	357	2	S09265	Ig alpha chain C r
1198	77	5.0	392	2	G70146	methionine adenosy
1199	77	5.0	405	1	G2MSBM	Ig gamma-2b chain
1200	77	5.0	412	2	D72364	conserved hypothet
1201	77	5.0	468	2	A41242	interleukin-6 rece
1202	77	5.0	490	2	F87843	conserved hypothet
1203	77	5.0	497	2	T14433	reproductive merlia
1204	77	5.0	499	2	B64069	fructose phosphotr
1205	77	5.0	516	2	T49422	RAD57 related prot
1206	77	5.0	569	2	A46462	T cell activation
1207	77	5.0	595	2	A10042	thiol,disulfide in
1208	77	5.0	613	2	T27528	hypothetical precu
1209	77	5.0	664	2	JC7990	acetylcholinestera
1210	77	5.0	700	2	C86296	hypothetical prote
1211	77	5.0	726	2	T33998	hypothetical prote
1212	77	5.0	772	2	I48747	semaphorin D - mou
1213	77	5.0	803	2	T04190	subtilisin-like pr
1214	77	5.0	825	2	T29634	hypothetical prote
1215	77	5.0	829	2	I46536	Ksp-cadherin - rab
1216	77	5.0	986	2	A29646	invasin - Yersinia
1217	77	5.0	991	1	I78843	receptor protein-t
1218	77	5.0	1087	1	S41797	cellulose 1,4-beta
1219	77	5.0	1802	2	S69703	HKR1 protein precu
1220	77	5.0	3034	2	T14119	seven-pass transme
1221	76.5	5.0	315	2	T37442	hypothetical prote
1222	76.5	5.0	317	2	S58689	EBV gp42.ps/hr pro
1223	76.5	5.0	353	2	D87539	hypothetical prote
1224	76.5	5.0	357	2	S11133	class I histocompa
1225	76.5	5.0	144	2	S54231	Ig mu heavy chain
1226	76.5	5.0	139	2	S54428	Ig mu heavy chain
1227	76.5	5.0	115	2	S03482	class I histocomp
1228	76.5	5.0	262	2	I37243	class II histocomp
1229	76.5	5.0	224	2	A25925	CMRF-35 antigen -
1230	76.5	5.0	220	2	T01562	hypothetical prote
1231	76.5	5.0	144	2	S54231	Ig mu heavy chain
1232	76.5	5.0	139	2	S54428	Ig mu heavy chain
1233	76.5	5.0	362	2	S11133	class I histocompa
1234	76.5	5.0	362	2	I61861	MHC HLA-B44.2 chai
1235	76.5	5.0	365	2	S25415	class I histoc
1236	76.5	5.0	365	2	S77963	MHC class I histoc
1237	76.5	5.0	365	2	I54416	HLA-AW24
1238	76.5	5.0	370	2	I54493	MHC class I histo
1239	76.5	5.0	418	2	H84351	hypothetical prote
1240	76.5	5.0	419	2	E96687	hypothetical prote
1241	76.5	5.0	448	2	S56073	MHC class I histoc
1242	76.5	5.0	456	2	A38445	opaque-2 protein -
1243	76.5	5.0	510	2	T38221	EV12B protein prec
1244	76.5	5.0	549	2	S45571	extensin homolog F
1245	76.5	5.0	574	2	S04845	hypothetical serin
1246	76.5	5.0	621	2	F73356	nuclear factor I-C
1247	76.5	5.0	671	2	I38467	serine/threonine p
1248	76.5	5.0	709	2	C83934	low density lipopr
1249	76.5	5.0	771	2	S38883	methyl-accepting c
1250	76.5	5.0	839	2	S25814	polyribonucleotide
1251	76.5	5.0	849	2	T04859	hypothetical prote
1252	76.5	5.0	938	2	T04242	Ig mu heavy chain
1253	76.5	5.0	1041	2	AF1772	membrane-bound imm
1254	76.5	5.0	1248	2	S55862	Ig heavy chain v r
1255	76.5	5.0	2397	2	C89074	Ig heavy chain v r
1256	76.5	5.0	2809	2	A55535	pregnancy-specific
1257	76	4.9	118	2	T30213	G-cadherin - sea u
1258	76	4.9	120	2	PH1498	versican precursor
1259	76	4.9	133	2	PL0084	autolysin [importe
1260	76	4.9	138	2	PS0089	probable membrane
1261	76	4.9	139	2	I45927	internalin-like pr
1262	76	4.9	140	2	S31810	abdominal segment
1263	76	4.9	141	2	S31678	CD8 antigen - huma
1264	76	4.9	142	2	S54241	CTLA-4 precursor -
1265	76	4.9	192	2	I39464	Ig kappa chain pre
1266	76	4.9	223	2	I55654	MHC class II prote
1267	76	4.9	233	2	I66696	MHC class II
1268	76	4.9	234	2	I55007	Ig kappa chain pre
1269	76	4.9	238	2	S01320	MHC class II
1270	76	4.9	241	2	I71907	Ig kappa chain pre
1270	76	4.9	264	1	HLMSE1	H-2 class II histo

Seq	%	%	Len	N	Accession	Description
1271	76	4.9	264	1	H1MSEB	H-2 class II histo
1272	76	4.9	264	2	A30529	H-2 class II histo
1273	76	4.9	268	2	C87579	TonB-dependent rec
1274	76	4.9	269	2	S57494	flagellar basal-bo
1275	76	4.9	354	2	T38306	T-cell receptor al
1276	76	4.9	362	2	A45897	guanine nucleotide
1277	76	4.9	363	2	S07113	MHC class I histoc
1278	76	4.9	365	2	I38720	class I histocompa
1279	76	4.9	374	1	A39878	hFcRn - human
1280	76	4.9	397	2	B27496	Fc gamma (IgG) rec
1281	76	4.9	444	1	PC4436	proteinase inhibit
1282	76	4.9	449	1	B43698	monoclonal antibod
1283	76	4.9	474	1	S15590	paired box transcr
1284	76	4.9	475	1	S01321	Ig heavy chain - h
1285	76	4.9	500	1	ITHUC1	Ig gamma-2b chain
1286	76	4.9	550	2	AI15522	complement C1 inhi
1287	76	4.9	651	2	A96591	NPK1-related prote
1288	76	4.9	669	2	I38029	matrix metalloprot
1289	76	4.9	711	2	AD0901	polynucleotide pho
1290	76	4.9	720	2	G97229	pullulanase [impor
1291	76	4.9	753	2	T24869	hypothetical prote
1292	76	4.9	798	2	H87271	TonB-dependent rec
1293	76	4.9	841	2	JC5894	class II histocomp
1294	76	4.9	846	2	C82135	killer cell inhibi
1295	76	4.9	906	2	G90281	chitinase VC1952 [
1296	76	4.9	1072	2	S76888	conserved hypothet
1297	76	4.9	1175	2	T46124	hypothetical prote
1298	75.5	4.9	115	2	A25924	Ig kappa chain pre
1299	75.5	4.9	118	1	S37201	Ig heavy chain V r
1300	75.5	4.9	131	1	KVMSM6	Ig kappa chain pre
1301	75.5	4.9	138	1	I46634	Ig heavy chain V r
1302	75.5	4.9	153	2	S31700	rearranged T-cell
1303	75.5	4.9	185	2	S37479	T-cell receptor al
1304	75.5	4.9	215	2	JE0244	Ig kappa chain NIG
1305	75.5	4.9	261	2	S17889	Ig kappa chain NIG
1306	75.5	4.9	269	2	T42919	class II histocomp
1307	75.5	4.9	322	2	PS0019	protein tio - atel
1308	75.5	4.9	333	2	AF0407	lipoprotein [impor
1309	75.5	4.9	343	2	S25644	Ig mu chain C regi
1310	75.5	4.9	345	2	HLCHB4	MHC class I histoc
1311	75.5	4.9	349	2	T42965	glycoprotein - ate
1312	75.5	4.9	354	2	S18197	class I histocompa
1313	75.5	4.9	355	2	T28152	MHC class I histoc
1314	75.5	4.9	357	2	I36966	MHC class I protei
1315	75.5	4.9	362	2	JH0538	class I histocompa
1316	75.5	4.9	408	2	S42493	opaque 2 protein -
1317	75.5	4.9	411	2	AI11161	flagellar hook pro
1318	75.5	4.9	411	2	AI11520	flagellar hook pro
1319	75.5	4.9	417	2	A81248	UDP-N-acetylglucos
1320	75.5	4.9	457	2	A27449	T-cell surface gly
1321	75.5	4.9	463	2	C86341	F9H16.15 protein -
1322	75.5	4.9	472	2	T24316	hypothetical prote
1323	75.5	4.9	475	2	S47861	hypothetical prote
1324	75.5	4.9	477	2	T46917	mei-1 protein - Ca
1325	75.5	4.9	495	2	S76967	hypothetical prote
1326	75.5	4.9	502	2	A48679	brevican precursor
1327	75.5	4.9	555	2	T21028	differentiated ker
1328	75.5	4.9	760	2	P86387	probable Pto kinas
1329	75.5	4.9	778	2	P84237	Ig lambda chain r
1330	75.5	4.9	778	2	T48897	Htr4 transducer [i
1331	75.5	4.9	784	2	T20074	transducer protein
1332	75.5	4.9	786	2	T16509	hypothetical prote
1333	75.5	4.9	796	2	T21460	hypothetical prote
1334	75.5	4.9	829	2	D71485	probable adenylate
1335	75.5	4.9	883	2	S57653	hypothetical prote
1336	75.5	4.9	947	2	T23107	hypothetical prote
1337	75.5	4.9	1019	2	T13039	tyrosine kinase re
1338	75.5	4.9	1045	2	S60571	integrin alpha v c
1339	75.5	4.9	1118	2	H97298	subtilisin like pr
1340	75.5	4.9	1125	1	S57846	protein-tyrosine k
1341	75.5	4.9	1152	1	AC1347	probable peptidog
1342	75.5	4.9	1433	1	A36734	bacillopeptidase F
1343	75.5	4.9	1530	2	I45944	neurexin I-alpha -

Seq	%	%	Len	N	Accession	Description
1344	75.5	4.9	2329	2	S44625	C50C3.6 protein -
1345	75	4.9	115	2	S13726	Ig lambda chain V
1346	75	4.9	121	2	S31602	Ig heavy chain r
1347	75	4.9	132	2	S11740	Ig heavy chain pre
1348	75	4.9	132	2	S26882	Ig kappa chain V r
1349	75	4.9	135	2	S03537	class I histocompa
1350	75	4.9	135	2	C39371	Ig V-region-like B
1351	75	4.9	137	2	B47159	Ig heavy chain V r
1352	75	4.9	140	2	E34903	Ig heavy chain pre
1353	75	4.9	391	2	PH1484	Ig heavy chain V r
1354	75	4.9	301	2	S29690	Ig heavy chain VDJ
1355	75	4.9	321	2	A60548	synaptophysin - Pa
1356	75	4.9	321	2	E81668	conserved hypothet
1357	75	4.9	344	2	S39601	class I histocompa
1358	75	4.9	354	1	A46393	GTP-binding protei
1359	75	4.9	355	2	I80171	class I histocompa
1360	75	4.9	358	2	F70577	probable lipoprote
1361	75	4.9	363	2	S03537	hypothetical prote
1362	75	4.9	372	2	C39371	class I histocompa
1363	75	4.9	373	2	S43455	Ig alpha chain C r
1364	75	4.9	387	2	A37986	Ig mu chain C regi
1365	75	4.9	391	2	I58876	hypothetical prote
1366	75	4.9	406	1	G2MS11	interleukin-6 rece
1367	75	4.9	429	2	A29849	Ig gamma-2b chain
1368	75	4.9	438	1	T21296	interleukin-6 rece
1369	75	4.9	451	2	B71612	hypothetical prote
1370	75	4.9	462	2	D88550	ATP binding casset
1371	75	4.9	462	2	B54774	protein ZC84.6 [im
1372	75	4.9	474	1	AC1533	hypothetical prote
1373	75	4.9	474	1	S59310	probable receptor
1374	75	4.9	532	2	S56032	probable gtpase ac
1375	75	4.9	643	2	JC4566	secreted protein c
1376	75	4.9	645	2	T27852	a-agglutinin core
1377	75	4.9	645	2	A41258	hypothetical prote
1378	75	4.9	695	2	D96949	chitinase (EC 3.2.
1379	75	4.9	724	2	T39954	probable membrane
1380	75	4.9	725	2	E96631	surface protein (L
1381	75	4.9	825	2	S43455	probable membrane
1382	75	4.9	881	2	C39371	probable cysteine
1383	75	4.9	881	2	S03537	Ig mu chain C regi
1384	75	4.8	1104	2	T09058	Ig gamma-2a chain
1385	75	4.9	1104	2	I50703	Ig heavy chain V r
1386	75	4.9	1386	1	PH1493	Ig lambda chain V
1387	74.5	4.9	1472	1	B47159	Ig upsilon chain -
1388	74.5	4.9	1474	2	E34903	Ig heavy chain V r
1389	74.5	4.9	3973	2	PH1002	Ig heavy chain V r
1390	74.5	4.8	95	2	C44151	Ig heavy chain V r
1391	74.5	4.8	106	2	S25177	Ig kappa chain V r
1392	74.5	4.8	112	2	B71612	Ig gamma-2a chain
1393	74.5	4.8	144	2	S12244	Ig kappa chain - m
1394	74.5	4.8	219	2	S52028	MHC class I histoc
1395	74.5	4.8	248	2	A54295	Ig alpha chain C r
1396	74.5	4.8	261	2	D42526	interferon alpha/b
1397	74.5	4.8	264	2	S20690	interferon alpha/b
1398	74.5	4.8	276	2	B30582	BSR protein - vacc
1399	74.5	4.8	317	2	S29360	interferon alpha/b
1400	74.5	4.8	331	2	B31790	31.6K hypothetical
1401	74.5	4.8	331	2	B45831	MHC class II histo
1402	74.5	4.8	339	2	S09264	MHC class I histoc
1403	74.5	4.8	341	2	S59501	Fc gamma (IgG) rec
1404	74.5	4.8	342	2	S09264	Ig heavy chain V r
1405	74.5	4.8	344	2	A46529	Ig gamma chain C r
1406	74.5	4.8	360	2	B28967	T-cell surface gly
1407	74.5	4.8	362	2	A27638	probable cysteine
1408	74.5	4.8	371	2	I38421	Ig alpha chain C r
1409	74.5	4.8	383	2	A53908	MHC class I histoc
1410	74.5	4.8	419	2	T21946	gene HLA B-1519 pr
1411	74.5	4.8	445	2	S14508	brevican precursor
1412	74.5	4.8	473	2	T21744	asparagine-rich pr
1413	74.5	4.8	515	2	E84853	hypothetical prote
1414	74.5	4.8	528	2	I39073	hypothetical prote
1415	74.5	4.8	528	2	PC4025	interferon alpha-b
1416	74.5	4.8	552	1	S35703	intercellular adhe
	74.5	4.8				colony-stimulating

Seq	%A	%B	Len	N	Accession	Description
1417	74.5	4.8	552	1	A31401	macrophage colony-
1418	74.5	4.8	590	2	A44068	cell pattern forma
1419	74.5	4.8	643	2	AC2199	phosphoenolpyruvat
1420	74.5	4.8	710	2	S63598	cyclomaltodextrin
1421	74.5	4.8	761	1	IJBODE	desmocollin 1a - b
1422	74.5	4.8	806	2	E69424	hypothetical prote
1423	74.5	4.8	812	1	MMECOF	outer membrane ush
1424	74.5	4.8	839	1	IJBODF	desmocollin 1b pre
1425	74.5	4.8	869	2	T44440	chitinase (EC 3.2.
1426	74.5	4.8	883	2	S49126	brevican precursor
1427	74.5	4.8	912	2	A54423	brevican precursor
1428	74.5	4.8	952	2	T32836	hypothetical prote
1429	74.5	4.8	988	2	I50611	protein-tyrosine k
1430	74.5	4.8	992	2	A39931	protein-tyrosine k
1431	74.5	4.8	1000	2	S18827	Flt3 protein - mou
1432	74.5	4.8	1116	2	S63397	probable membrane
1433	74.5	4.8	1138	1	S24066	protein-tyrosine k
1434	74.5	4.8	1441	2	GNVUSV	adhesin homolog lm
1435	74.5	4.8	1582	2	AB1730	M polyprotein prec
1436	74.5	4.8	1601	2	AB1153	hypothetical prote
1437	74.5	4.8	3029	2	S76109	hypothetical prote
1438	74	4.8	115	2	PL0238	Ig heavy chain v r
1439	74	4.8	117	2	PL0237	Ig heavy chain v r
1440	74	4.8	118	2	PL0235	Ig heavy chain v r
1441	74	4.8	119	2	PL0231	Ig heavy chain v r
1442	74	4.8	119	2	PH1505	Ig heavy chain v r
1443	74	4.8	120	2	G28195	Ig heavy chain v6
1444	74	4.8	123	2	S24693	Ig heavy chain v r
1445	74	4.8	133	2	S34010	Ig heavy chain v r
1446	74	4.8	135	2	I46643	rearranged T-cell
1447	74	4.8	135	2	PL0100	Ig heavy chain pre
1448	74	4.8	144	2	S54204	Ig mu heavy chain
1449	74	4.8	228	2	S03050	Ig gamma chain (cl
1450	74	4.8	229	2	I45936	MHC lymphocyte ant
1451	74	4.8	237	2	B28043	MHC class II histo
1452	74	4.8	246	2	I50094	MHC class II beta
1453	74	4.8	248	2	S35076	class II histocomp
1454	74	4.8	255	2	I47092	MHC OVAR-DQ-ALPHA-
1455	74	4.8	261	2	A55242	MHC class II histo
1456	74	4.8	277	2	AB1390	hypothetical cell
1457	74	4.8	329	1	A48754	B7-2 antigen - hum
1458	74	4.8	332	2	T45770	hypothetical prote
1459	74	4.8	347	2	S09274	Ig alpha chain C r
1460	74	4.8	365	2	JH0534	lactocepin (EC 3.4
1461	74	4.8	365	2	I84432	class I histocompa
1462	74	4.8	386	2	T19940	MHC class I precei
1463	74	4.8	396	2	T01049	hypothetical prote
1464	74	4.8	401	2	AH0364	hypothetical prote
1465	74	4.8	404	2	A44833	probable HlyD fami
1466	74	4.8	409	2	AB3624	lactocepin (EC 3.4
1467	74	4.8	463	2	T14884	acriflavin resista
1468	74	4.8	472	2	G87068	hypothetical prote
1469	74	4.8	492	2	B86911	pyruvate kinase [i
1470	74	4.8	520	2	S62521	probable penicilli
1471	74	4.8	521	2	S54266	hypothetical prote
1472	74	4.8	547	1	S28904	glycoprotein gC -
1473	74	4.8	571	2	T08930	intracellular adhe
1474	74	4.8	609	2	JQ0703	hypothetical prote
1475	74	4.8	609	2	S11481	glycogen(starch) s
1476	74	4.8	619	2	A43361	glycogen(starch) s
1477	74	4.8	726	2	T40790	Ets-related transc
1478	74	4.8	734	2	H65106	probable permease
1479	74	4.8	734	2	H85979	polyribonucleotide
1480	74	4.8	734	2	E91134	polynucleotide pho
1481	74	4.8	737	2	T46101	ABC transporter-li
1482	74	4.8	753	2	G02173	semaphorin III fam
1483	74	4.8	791	2	T16031	receptor tyrosine
1484	74	4.8	898	2	S47489	unknown protein F1
1485	74	4.8	1020	2	H96793	HPI layer surface
1486	74	4.8	1036	2	A29832	BH-protocadherin P
1487	74	4.8	1072	2	T00041	BH-protocadherin P
1488	74	4.8	1141	2	E89824	hypothetical prote
1489	74	4.8	1200	2	T00042	BH-protocadherin P
1490	74	4.8	1251	2	T21389	hypothetical prote
1491	74	4.8	1353	2	T19691	hypothetical prote
1492	74	4.8	1417	2	H90670	probable invasin |
1493	74	4.8	1417	2	D85521	probable adhesin e
1494	74	4.8	1483	2	C97012	probably cellulose
1495	74	4.8	1962	2	A32634	lactocepin (EC 3.4
1496	74	4.8	2508	2	S61441	surface-associated
1497	74	4.8	3705	2	AD0123	probable autotrans
1498	74	4.8	3716	2	B70969	probable PPE prote
1499	74	4.8	4436	2	E71086	hypothetical prote
1500	73.5		116	1	HVMS1B	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S56749

junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130,'FDKDXTIYLNXY','LT',206,'X'
A;Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI000000000DC1; GB:AAD42050; NID:9532679?; PI
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 1-299 <OZA>
A;Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI0001468C7; UNIPARC:UPI0001468CD; UNIPARC:UPI0001468D1;
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

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Best Local Similarity   100.0%;
Matches  299;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MGTKAQVERKLLCLFILAILLCSIALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGTKAQVERKLLCLFILAILLCSIALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy  121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy  181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy  241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
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RESULT 2

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JC7780
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C;Accession: JC7780
R;Thoelen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A;Reference number: JC7780
A;Contents: Liver
A;Accession: JC7780
A;Molecule type: mRNA
A;Residues: 1-365 <THO>
C;Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Qy    Query Match    12.7%;    Score 196;    DB 2;    Length 365;
      Best Local Similarity    27.1%;    Pred. No. 5.5e-07;
      Matches    74;    Conservative    42;    Mismatches    109;    Indels    48;    Gaps    14;

Qy      14 LFILAILLLCSLA--LGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSSPR----------VEWKFD 65
              :  :||||  |: |||||||:|||||::|: |:| |||:|| |  | ||            ||| |
Db       3 LLLRFLLLCGVADFTRGLSLTTPEQMIEKAKGETAYLPCKFT--LGPEDQPLIDIEWLLS 60

Qy      66 QGDTTR----LVCYN-NKITASY----EDRVTF----LPTGITFKSVTR----EDTGTYTC 109
             |||:|     | |   | |: |     ||| ||    | | | |||:||    |||||| |
Db      61 PADNQKVDQVIILYSGDKIYQDLKGRVHFTSNDLKSGDASINVTNLQLSDTGTYQC 120

Qy     110 MVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFK- 168
            ||||||||||||||| ||: ||| | | |||||:|||:|||||:|||||: ||||||||
Db     110 MVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFK- 168

Qy     121 KVKKAPG--VGNKIQLTVLVKPSGIRCYVDGSEIGNDPKLKCEPKEGSLPLRVEWQKL 178
            |: | |    ||||:|||||:| |  | |  || || |  | || |  | ||||:|:|
Db     121 KVKKAPG--VGNKIQLTVLVKPSGIRCYVDGSEIGNDPKLKCEPKEGSLPLRVEWQKL 178

Qy     169 -DGIVMPTNPKSTRAFSNSSYVLNPFTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAV 227
              || |:| |||||| ||||||||| ||||||||||||||||||||||||||||||||||
Db     169 -DGIVMPTNPKSTRAFSNSSYVLNPFTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAV 227

Qy     179 SDSQKLPT----------SWLPEMTSPVISVKNASAEYSGTYTCTVRNRVGSDQC--LL 225
            ||| ||             ||||| : | | |  | | ||| ||||| |||  |  ||
Db     179 SDSQKLPT----------SWLPEMTSPVISVKNASAEYSGTYTCTVRNRVGSDQC--LL 225

Qy     228 RMEAV----ERNGVIVAAV----LVTLILLILGILVF 255
            |: ||    ||||||:|||    ||||:|||||:| |
Db     226 RLDVVPPSNRAGTIAGAVIGTLLALVLIALIVF 258
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```
RESULT 3
I38346
elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38346
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: I38346
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-7962 <RES>
A;Molecule type: mRNA
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PI
A;Gene: GDB:TTN
A;Genetics:
C;Genetics:
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31

Qy    Query Match    12.3%;    Score 189.5;    DB 2;    Length 7962;
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      Matches    70;    Conservative    39;    Mismatches    115;    Indels    47;    Gaps    11;

Qy      42 ENNPVKLSCAYSGFSSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTR 101
            ||||| |||: |  | | |  |||||  || |||  :|| :|| |  | ||| | |:
Db    3043 QGESIQLECKISGSPEIKVSWFRNDSELHESWKYN----MSFINSVALL----TINEASA 3094

Qy     102 EDTGTYTCMVSEEGGNSYGEV-----SKPTVNIPSSATIGNRAVLTCSEQ 156
            ||||| ||:||| |||||||      ||||||||||||||||||||||||
Db    3095 EDSGDYIC----EAHNGVGDASCSTALTVKAPPVETQKPS----PVGALKGSDVILQC-EI 3146
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RESULT 4
I49583
differentiation antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A;Reference number: I49583
J. Immunol. 151, 175-187, 1993
A;Title: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characteriza
A;Accession: I49583
A;Reference number: I49583; MUID:93315834; PMID:8100843
A;Molecule type: mRNA
A;Residues: 1-862 <RES>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:P35329; UNIPARC:UPI000027DD2; GB:L16928; NID:g348965; PIDN:I
C;Genetics:
A;Gene: CD22

Qy    Query Match    11.8%;    Score 181.5;    DB 2;    Length 862;
      Best Local Similarity    29.0%;    Pred. No. 1.7e-05;
      Matches    75;    Conservative    32;    Mismatches    85;    Indels    67;    Gaps    15;

Qy      22 CSLALGSV-TVHSSEPEVRIPENNP----------VKLSC--AYSGFSSSPRVEWKFDQGDGT 69
            || | ||  |||||||||||||||           ||||   |||| | ||||||||||| |
Db       1 CSWALPVILNVHYARPDVKVLKVSPASEIRAGQRVLLQCDFAESNPAEVRRFWK-----L 126

Qy      70 TRLVCYNNKITASYEDRVTFLPTGITFKSVTREDGTYTCMVSEEGGNSYGEVKVKR---L 126
            |||||||||||||||||||||||||||||||| | |||||||||||||||||||||
Db     506 CSWALPVILNVHYARPDVKVLKVSPASEIRAGQRVLLQCDFAESNPAEVRRFWK----- 559

Qy     127 IVLVPPSKPTVNIPSSATI--GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAF 183
            ||||||||||||||||||   |||||||||||| |||  ||||||||||||||||||||
Db     560 -----KNGSLV--QEGRY-----LSFGSVSPEDSGNYNCMVN----NSIGETLSQWNL 602

Qy     184 SNSSYVLNPFTGELVFDPLSASDTGEYSCEARNGYGT-----PMTSNAVRMEAVERNNGVI 239
            ||||||||| ||||||||||||||||||||||| | |      | | | |:| |  | |
Db     603 QVLYAPRLRVSISPGDHVMEGKKATLSC-ESDANPISQYTW--------F 645

Qy     240 VAAVLVTLILLILGILVFGIW 258
            |||||||||||||||||||||
Db     646 DSSGQDLHSSGQKLRLEPLEVQHTGSYRCKGTNGIGTGESPPST----LTVYYSPFIGKR 702

Qy     267 DRTKKGT-------SSKKVIYSQPSARSEGEF 291
            | | |          | |  :| | | | | |
Db     703 VALGLG--FCLTICILAIW 719
```

```
RESULT 5
A46512
CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A46512
R;Torres, R.M.; Law, C.L.; Santos-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse,
J. Immunol. 149, 2641-2649, 1992
A;Title: Identification and characterization of the murine homologue of CD22, a B lympho
A;Reference number: A46512; MUID:93017867; PMID:1401903
A;Accession: A46512
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-868 <TOR>
A;Cross-references: UNIPARC:UPI00017C631
A;Experimental source: B cell lymphoma 38C13
A;Note: sequence extracted from NCBI backbone (NCBIP:1161156)
```

(Left column continuation)

```
Qy     157 DGSPSPEYTWFKDGIVMPTNPK---STRAFSNSSYVLNPFTGELVFDPLSASDTGEYSCE 213
            |||| || |||||||||||||    |||||||||||||||||||||||||||||||||
Db    3147 SGTPPPEVVWVDRKQVRNSKKFKITSKHFDTNLHLLN----------LEASDGEYHCK 3196

Qy     214 ARNGYGTPMTSNAVRMEAVERNV-------GVIVAAVLVTLILLGILVFGIWFAYSRGHF 266
            | |||||||||||||||||||||        ||| ||||||||||||||||| | | | |
Db    3197 ATNEVGSDTGCSCSVKFKEPPRFVKLLSDTGTLIGDAVELRAIVEGEQPISVVWLKDRGEV 3256

Qy     267 DRTKKGT-------SSKKVIYSQPSARSEGEF 291
            | | |          | |  :| | | | | |
Db    3257 IRESENTRISFIDNIATLQLGSPEASNSGKY 3287
```

RESULT 6
JC2457
vascular cell adhesion protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2457
R;Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
A;Title: Cloning and expression kinetics of porcine vascular cell adhesion molecule.
A;Reference number: JC2457; MUID:94271236; PMID:7516159
Biochem. Biophys. Res. Commun. 201, 805-812, 1994
A;Accession: JC2457
A;Molecule type: mRNA
A;Residues: 1-538 <TSA>
A;Cross-references: UNIPROT:Q28939; UNIPARC:UPI000000881155; EMBL:U08351; NID:g474382; PID
A;Cross-references: UNIPROT:Q28939;
C;Keywords: Glycoprotein; transmembrane protein #status predicted <TMM>
F;497-517/Domain: transmembrane #status predicted <TMM>
F;75,157,271,330,360/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
Best Local Similarity 29.3%; Pred. No. 1.7e-05;
Matches 76; Conservative 32; Mismatches 84; Indels 67; Gaps 16;
Score 181.5; DB 2; Length 868;

```
Qy  22 CSLALGSV-TVHSSEPEVRIPENNP------VKLSC--AYSGFSSPRVEWKFPDQGDT  69
          |:|:|  :|||::  ||::|:
Db 512 CSWALPVILNVHYAPRDVKVLKVSPASEIRAGQRVLLQCDFAESNPAEVRFFWK----  565

Qy  70 TRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVK--L  126
          |:|:   :    ::|   |:  || ||::|||||||||||||||||||||||||  |
Db 566 ----KNGSLV--QEGRY-----LSFGSVSPEDSGNYNCMVN----NSIGETLSQAWNL  608

Qy 127 IVLVPPSKPTVN-IFSSATI-GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAF  183
          |||   |  |:  |    |:| |||||||||||||||| ||||||||||||||||||||
Db 609 QVLYAPRLRVSIIPGDHVMEGKKATLSC-ESDANPPISQYTW------P  651

Qy 184 SNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT----PMTSNAVRMEAVERNVGVI  239
          |||||||||||||||||||||||||||||||||||     ||||||||||||||||||
Db 652 DSSGQDLHSSGQKLRLEPLEVQHTGSYRCKGTNGIGTGESSPPST---LTVVYSPETIGKR  708

Qy 240 VAAVLVTLILLGILVFGIW  258
          |||||||||||||||||||
Db 709 VALGLG--FCLTIFILAIW  725
```

RESULT 7
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N;Alternate names: B-cell membrane protein CD22
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0371; I56171
R;Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J;J. Exp. Med. 173, 137-146, 1991
A;Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell intera
A;Reference number: JH0371; MUID:91086838; PMID:1985119
A;Accession: JH0371
A;Molecule type: mRNA
A;Residues: 1-847 <WIL>
A;Cross-references: UNIPROT:O60926; UNIPARC:UPI0000161B10; GB:X59350; NID:g336090; PIDN:C
A;Experimental source: B lymphocyte
A;Note: the authors translated the codon AAT for residue 358 as Met
R;Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J;Immunol. 150, 5013-5024, 1993
A;Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A;Reference number: I56171; MUID:93267103; PMID:8496602
A;Accession: I56171
A;Molecule type: DNA
A;Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <WIL2>
A;Cross-references: UNIPARC:UPI0000006BB4A; GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:
A;Status: translated from GB/EMBL/DDBJ
C;Genetics:
A;Gene: GDB:CD22
A;Map position: 19q13.1-19q13.1
A;Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
A;Cross-references: GDB:127545; OMIM:107266
C;Genetics:
A;Gene: GDB:CD22
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F;346-398/Domain: immunoglobulin homology <IMM1>
F;609-661/Domain: immunoglobulin homology <IMM2>
F;688-706/Domain: transmembrane #status predicted <TRA>
F;764,789/Binding site: phosphate (Thr) (covalent) #status predicted
F;764,789/Binding site: carbohydrate (Asn) (coval

Query Match
Best Local Similarity 21.5%; Pred. No. 1.5e-05;
Matches 70; Conservative 45; Mismatches 100; Indels 110; Gaps 12;
Score 179; DB 2; Length 538;

```
Qy  31 VHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW---KFDQGDTTRLVCYNNKITASYEDRVT   88
Db  29 VTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVT    88

Qy  89 FLPTGITFKSVTREDTGTYTCMVSEEGGNSYG---EVKVKLIVLVPPSKPTVNIPSSATI  145
Db 508 VRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEK------NGRLL  550

Qy 146 --GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKST  180
Db 551 GKESQLNFDSISPEDAGSYSCWVN---NSIGQTASKAWTLEVLYAPRLRVSMSPGDQV  606

Qy 181 RAFSNSSY  188
Db 607 MEGKSATLTC-ESDANPPVSHYTWFD  649

Qy 189 VLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLV--  245
Db 650 KVQHSGAYWCQGTNSVGKGRSPLSTLVYYSPETIGRRVAVGLGSCLAILIL--AICGL  706

Qy 246 --TLIL--LGILVFGIWFAYSRGHF  266
Db 707 ------KLQRRWKRTQSQQGLQENSSGQS  729

Qy 258 WFAYSRGHFDRTKKGTGSSKKVIYSQPSARS  287
```

RESULT 8
T17346
hypothetical protein DKFZp586O1624.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17346
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;submitted to the Protein Sequence Database, September 1999

Query Match
Best Local Similarity 25.6%; Pred. No. 2.7e-05;
Matches 69; Conservative 42; Mismatches 100; Indels 59; Gaps 12;
Score 178.5; DB 2; Length 847;

```
Qy  29 VTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVT  88
Db 508 VRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEK------NGRLL  550

Qy  89 FLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVK----LIVLVPPSKPTVNIPSSATI  145
Db 551 GKESQLNFDSISPEDAGSYSCWVN---NSIGQTASKAWTLEVLYAPRLRVSMSPGDQV  606

Qy 146 --GNRAVLTCSEQDGSPP-SEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPL  202
Db 607 MEGKSATLTC-ESDANPPVSHYTWFD-------------WNNQS--LPHHSQKLRLEPV  649

Qy 203 SASDTGEYSCEARNGYG---TPMTSNAV--RMEAVERNNGVIVAAVLVTLILLGILVFGI  257
Db 650 KVQHSGAYWCQGTNSVGKGRSPLSTLVYYSPETIGRRVAVGLGSCLAILIL--AICGL  706

Qy 258 WFAYSRGHFDRTKKGTGSSKKVIYSQPSARS  287
Db 707 ------KLQRRWKRTQSQQGLQENSSGQS  729
```

A;Reference number: Z18727
A;Accession: T17346
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-483 <DUE>
A;Cross-references: UNIPROT:Q9UFI4; UNIPARC:UPI00000726A2; EMBL:AL117666
A;Experimental source: adult uterus; clone DKFzp58601624
C;Genetics:
A;Note: DKFzp58601624.1

Qy   Best Local Similarity   24.6%;
        Matches   68;   Conservative   32;   Mismatches 112;   Indels   64;   Gaps   12;

RESULT 9
A35648
B-cell adhesion protein CD22 alpha splice form precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 15-Mar-2004
C;Accession: A35648
R;Stamenkovic, I.; Seed, B.
Nature 345, 74-77, 1990
A;Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion.
A;Reference number: A35648; MUID:90231465; PMID:1691828
A;Accession: A35648
A;Molecule type: mRNA
A;Residues: 1-647 <STA>
A;Cross-references: GDB:127545; OMIM:107266
A;Gene: GDB:127545
C;Genetics:
A;Cross-references: UNIPARC:UPI000015270; GB:X52785; NID:g29778; PIDN:CAA36988.1; PID:g
A;Map position: 19q13.1-19q13.1
C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transmembr
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-510/Domain: extracellular #status predicted <EXT>
F;432-484/Domain: immunoglobulin homology <IMM>
F;511-529/Domain: transmembrane #status predicted <TMM>
F;530-647/Domain: intracellular #status predicted <CYT>
F;67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent) #st

RESULT 11
T23004
hypothetical protein F59F3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23004
R;Kershaw, J.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19651
A;Accession: T23004
A;Status: preliminary; translated from GB/EMBL/DDBJ

RESULT 10
T42405
sax-3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42405
R;Zallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple aspe
A;Reference number: 222160; MUID:98117250; PMID:9458046
A;Accession: T42405
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1273 <ZAL>
A;Cross-references: UNIPROT:O44928; UNIPARC:UPI00000080AA8; EMBL:AF041053; NID:g2804779; I
A;Note: sax-3
C;Genetics:
C;Function:
A;Description: sax-3 function is required at the time of axon guidance

A;Molecule type: DNA
A;Residues: 1-1227 <WIL>
A;Cross-references: UNIPROT:Q21038; UNIPARC:UPI0000077DBB; EMBL:Z68005; PIDN:CAA91990.1;
A;Experimental source: clone F59F3
C;Genetic8:
A;Gene: CESP:F59F3.1
A;Map position: X
A;Introns: 31/3; 58/1; 279/3; 429/2; 544/3; 638/2; 801/2; 887/1; 929/2; 1025/3; 1062/2;

Query Match   11.8%; Score 172.5; DB 2; Length 1227;
Best Local Similarity   24.0%; Pred. No. 0.00011;
Matches   65; Conservative   35; Mismatches 108; Indels   63; Gaps   9;

```
Qy   34 SEPEVRIPENNPVKLSCAYSGFSSP-RVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPT 92
            :||  |: |: || |||||   ||| | :| ::| ||| | : :  ||| ::|
Db  576 SEPSKIYEGDNVKLTCVFPLDSDDWSVSWRFEN------------SKSSDISSIPT 620

Qy   93 G-------------------IITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNI 139
                             ||| :||:|| || ||| ::|  : : :  :| :| |
Db  621 TTETEIKQYSKHLILNRDVTISFGTYTCVVNEDSEKLLETSIDVKAI---SKPSI-- 675

Qy  140 PSSATIGNRAVLTCSEQD----------GSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYV 189
               : || |: |   |           |  | |  |:||:
Db  676 -----TGGNSNAVVIVDYQYFEINCNMTGTPPVYQWFKDG------NPYTHGDVDGSILR 726

Qy  190 LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLIL 249
             ::    |  ||::|  |: || |  | :|: :  |    || : :   | : | | |
Db  727 VSRARGE------------DDGEFHCLATNRAGDKLNSIEVQVNNAPKG-SLFFYWFLALLLL 776

Qy  250 LGILVPGIWFAYSRGHPDRTKKGTSSKKVIY 280
          : | | ||| |: |: :|:  |: ::: :|
Db  777 ISIIAVFLLTCKLRASNRLTKQKDIALNTLY 807
```

RESULT 12
A58532
glial cell membrane glycoprotein LIG-1 precursor - mouse
C;Species: Mus musculus (house mouse)
A;Accession: A58532
R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A;Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in
R;Reference number: A58532; MUID:96394313; PMID:8798419
A;Accession: A58532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <SUZ>
A;Cross-references: UNIPROT:P70193; UNIPARC:UPI000029E57; GB:D78572; NID:g1545806; PIDN
A;Cross-references: proteoglycan amino-terminal homology <PAH>
F;36-61/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match   11.1%; Score 171; DB 2; Length 1091;
Best Local Similarity   23.5%; Pred. No. 0.00013;
Matches   67; Conservative   33; Mismatches 123; Indels   62; Gaps   12;

```
Qy   37 EVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITF 96
          |  | |:  | :|   |:  |: |  ||  ||    |     | |  :|:   |   |

Db  609 DIAIRTGTTARLECAATGHPNPQIAWQKDGG------------TDFPAARERRMHVMPDDVF 659
Qy   97 --KSVTREDTGTYTCMVSEEGGNSYGEVKVK--LIVLVPPSKPTVNIPSSATIGNRAVLT 152
Db  660 FITDVKIDDMGVSVSCTAQ---NSAGSVSANATILTVLETPSLAVPLEDRVVTVGETVAFQ 715
Qy  153 CSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSC 212
Db  716 C-KATGSPTIPRITWLKGG------RPLSL----TERHHFTPGNQLLVVQNMIDDAGRYTC 765
Qy  213 EARNGYGTPMTSNAVRMEAVE------RNVGVIVAAVLVTLILGILVFGIWFA------- 260
Db  766 EMSNPLGTERAHSQLSILPTPGCRKDGTTVGIFTIAVVCSIVLTSL----VWVCIIYQTR 821
Qy  261 ------------YSRGHFDRT------------------KKGTSSKKVIYSQPSARSEG 289
Db  822 KKSEEYSVTNTDETIVPPDVPSYLSSQGTLSDR------QETVRTEG 863
```

RESULT 13
C42632
cell adhesion molecule apCAM (clone d12) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: C42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: C42632; MUID:92263095; PMID:1585176
A;Accession: C42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-765 <MAY>
A;Note: sequence extracted from NCBI backbone (NCBIP:101351)
A;Experimental source: CNS
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   11.0%; Score 169.5; DB 2; Length 765;
Best Local Similarity   25.1%; Pred. No. 0.00011;
Matches   58; Conservative   36; Mismatches   86; Indels   51; Gaps   11;

```
Qy    9 RKLICLFIL------------------AILLCSIALGSVTVHSSEPEVRIPENNPVKLSCAYSG 54
Db  189 KKYLCDIIVIDTGETKDFYIDFPTVVKLPTIAL-PPTIHPDNPKV----GDEVKITCQARG 243
Qy   55 FSSSPRVEWKFDQGD---TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMV 111
Db  244 VPPP--TYQFKGKGDVMVTDEMV--NNGV--------LTINPLKTTDQATYTCIA 285
Qy  112 SEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI 171
Db  286 TNKGG--FAESSNTLDVKVPPIEDMEETYDAVSGQELTITCPAK-GDPEPSVIWKKDGP 342
Qy  172 ------------VMPTNPKSTRAFSNSSYVLNPTTGE-LVFDPLSASDTGEYSCEA 214
Db  343 QSASTDGIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTA 393
```

RESULT 14
B42632
cell adhesion molecule apCAM (clone d15) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: B42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: B42632; MUID:92263095; PMID:1585176
A;Accession: B42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-812 <MAY>

RESULT 15
A42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C;Species: Aplysia california (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: A42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-932 <MAY>
A;Experimental source: CNS
A;Cross-references: UNIPROT:Q9TWA6; UNIPARC:UPI00007FBFE
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   11.0%; Score 169.5; DB 2; Length 932;
Best Local Similarity 25.1%; Pred. No. 0.00014;
Matches   58; Conservative 36; Mismatches 86; Indels 51; Gaps 11;

Qy   9 RKLLCLFIL----------------------AILLLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSG 54
           :||||| :|:|| |:| |:|
Db   189 KKYLCDIIVIDTGETKDFYIDFTVVKLPTIAL-PPTIHPDNPKV---GDEVKITCQATG 243

Qy   55 FSSPRVEWKFDQGD---TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMV 111
           :|:||| || :|:| |:|| :|:
Db   244 VPPP--TYQFKKGDVMVTDEMV--NNGV---------LTINPLKTTDQATYTCIA 285

Qy   112 SEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGI 171
           :|| |:|| ||| :|||| ||| ||:|
Db   286 TNKGG--FAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAK-GDPEPSVIWKKDGP 342

Qy   172 ------VMPTNPKSTRAFSNSSYVLNPTTGE-LVFDPLSASDTGEYSCEA 214
                 :| |:|| |||| |||:
Db   343 QSASTDGIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTA 393

A;Cross-references: UNIPROT:Q9TWA5; UNIPARC:UPI0000007CEC1
A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:1013346)
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   11.0%; Score 169.5; DB 2; Length 812;
Best Local Similarity 25.1%; Pred. No. 0.00012;
Matches   58; Conservative 36; Mismatches 86; Indels 51; Gaps 11;

Qy   9 RKLLCLFIL----------------------AILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSG 54
           :||||| :|:|| |:| |:|
Db   189 KKYLCDIIVIDTGETKDFYIDFTVVKLPTIAL-PPTIHPDNPKV---GDEVKITCQATG 243

Qy   55 FSSPRVEWKFDQGD---TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMV 111
           :|:||| || :|:| |:|| :|:
Db   244 VPPP--TYQFKKGDVMVTDEMV--NNGV---------LTINPLKTTDQATYTCIA 285

Qy   112 SEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGI 171
           :|| |:|| ||| :|||| ||| ||:|
Db   286 TNKGG--FAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAK-GDPEPSVIWKKDGP 342

Qy   172 ------VMPTNPKSTRAFSNSSYVLNPTTGE-LVFDPLSASDTGEYSCEA 214
                 :| |:|| |||| |||:
Db   343 QSASTDGIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTA 393

Search completed: May 16, 2006, 07:03:28
Job time : 64 secs

OM protein search, using sw model
Run on: May 16, 2006, 07:03:43 ; Search time 187 Seconds
                                             702.536 Million cell updates/sec

Title:
Perfect score: 1544
Sequence: 1 MGTKAQVERKLCLFLAIL..............YSQPSARSEGEFKQTSSFLV 299
Scoring table: BLOSUM62
                      Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
Database :   A_Geneseq_21:*
                 Listing first 1500 summaries
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
                                        SUMMARIES

No.   Score   Match Length DB ID   Description

RESULT 1
ID   AAY23321 standard; protein; 299 AA.
DE   Amino acid sequence of the PRO301 polypeptide.
PN   WO927098-A2.
PD   03-JUN-1999.
PA   (GETH) GENENTECH INC.
PA   (SMIK) SMITHKLINE BEECHAM CORP.
     Query Match   100.0%;   Score 1544; DB 2; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 2
ID   AAW74464 standard; protein; 299 AA.
DE   F11 antigen protein sequence.
PN   WO902561-A1.
PD   21-JAN-1999.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 2; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 3
ID   AAY13364 standard; protein; 299 AA.
DE   Amino acid sequence of protein PRO301.
PN   WO914328-A2.
PD   25-MAR-1999.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   100.0%;   Score 1544; DB 3; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 4
ID   AAY76011 standard; protein; 299 AA.
DE   Human A33 receptor homologue, SEQ ID NO:189.
PN   WO955865-A1.
PD   04-NOV-1999.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   100.0%;   Score 1544; DB 3; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 5
ID   AAY76076 standard; protein; 299 AA.
DE   Human A33 receptor homologue, SEQ ID NO:331.
PN   WO955865-A1.
PD   04-NOV-1999.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   100.0%;   Score 1544; DB 3; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 6
ID   AAY70670 standard; protein; 299 AA.
DE   Human PRO301 protein.

PN   WO20015797-A2.
PD   23-MAR-2000.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 3; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 7
ID   AAB24405 standard; protein; 299 AA.
DE   Human PRO301 protein sequence SEQ ID NO:90.
PN   WO20032221-A2.
PD   08-JUN-2000.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 3; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 8
ID   AAY95344 standard; protein; 299 AA.
DE   Human PRO301 antitumour protein.
PN   WO20037638-A2.
PD   29-JUN-2000.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 9
ID   AAB80232 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   WO20104311-A1.
PD   18-JAN-2001.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 10
ID   AAM93577 standard; protein; 299 AA.
DE   Human polypeptide, SEQ ID NO:3365.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 11
ID   AAB56015 standard; protein; 299 AA.
DE   Skin cell protein, SEQ ID NO: 331.
PN   WO20069884-A2.
PD   23-NOV-2000.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 12
ID   AAB55950 standard; protein; 299 AA.
DE   Skin cell protein, SEQ ID NO: 189.
PN   WO20069884-A2.
PD   23-NOV-2000.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 13
ID   AAB31202 standard; protein; 299 AA.
DE   Amino acid sequence of human polypeptide PRO301.
PN   WO20007037-A2.
PD   21-DEC-2000.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 14
ID   AAU00823 standard; protein; 299 AA.
DE   Human immune response protein PRO301 (UNQ2664).
PN   WO20011991-A1.
PD   22-MAR-2001.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544; DB 4; Length 299;
     Best Local Similarity 100.0%;   Pred. No. 7.5e-105;

RESULT 15
ID   AAU12354 standard; protein; 299 AA.
DE   Human PRO301 polypeptide sequence.
PN   WO20014046-A2.

PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 16
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 17
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 18
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 19
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 20
ID AAE03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 21
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 22
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 4; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 23
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 24
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 25
ID ABG64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 26
ID ABG64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 27
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 28
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 29
ID ABB95449 standard; protein; 299 AA.
DE Human angiogenesis related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 30
ID ABU71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1544; DB 5; Length 299;
   Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 31
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1544; DB 6; Length 299;

Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 32
ID   ABU71465 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20021926659-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 33
ID   ABO25173 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030040014-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 34
ID   ABU81052 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030045311-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 35
ID   ABU71911 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US20030005530-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 36
ID   ABO1794 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20020197671-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 37
ID   ABU66752 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030036180-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 38
ID   ABU54367 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US20021322240-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 39
ID   ABU67291 standard; protein; 299 AA.
DE   Human secreted and transmembrane protein PRO301.
PN   US20030032063-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 40
ID   ABO47382 standard; protein; 299 AA.
DE   Human secreted/transmembrane polypeptide PRO301.
PN   US20030044639-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 41
ID   ABU59833 standard; protein; 299 AA.
DE   Novel secreted and transmembrane protein PRO301.
PN   US20030017563-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 42
ID   ABO25023 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein (PRO) #183.
PN   US20030036179-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 43
ID   ABU64519 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #23.
PN   US20020160374-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 44
ID   ABU72059 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20021177165-A1.
PD   28-NOV-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 45
ID   ABU67365 standard; protein; 299 AA.
DE   Human secreted protein PRO301.
PN   US20030023054-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 46
ID   ABU67160 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030032062-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 47
ID   ABO14885 standard; protein; 299 AA.
DE   Human secreted / transmembrane polypeptide PRO301.
PN   US20030036060-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 48
ID   ABU07736 standard; protein; 299 AA.
DE   Human A-33 related antigen PRO301.
PN   US20021822206-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 49
ID   AAO16451 standard; protein; 299 AA.
DE   Human junctional adhesion molecule 1 (huJAM1).
PN   WO20030508541-A2.
PD   30-JAN-2003.
PA   (ELIL) LILLY & CO ELI.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 50

ID   ABU67028 standard; protein; 299 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 51
ID   ABU69642 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 52
ID   ABU79802 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 53
ID   ABO14824 standard; protein; 299 AA.
DE   Human secreted / transmembrane polypeptide PRO301.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 54
ID   ADA45885 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 55
ID   ADA76316 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 56
ID   ADB29324 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 57
ID   ADA18966 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 58
ID   ADA61589 standard; protein; 299 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 59
ID   ADB19374 standard; protein; 299 AA.

DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 60
ID   ADB27915 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 61
ID   ADA86394 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 62
ID   ADB15958 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 63
ID   ADA47744 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003072215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 64
ID   ADA18180 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 65
ID   ABO32776 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 66
ID   ADA67539 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 67
ID   ADB30546 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 68
ID   ADA85842 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.

PN US20030082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 69
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 70
ID ADA79358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 71
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 72
ID ADB16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 73
ID ABO34836 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030049621-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 74
ID ABO16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 75
ID ADA91791 standard; protein; 299 AA.
DE Human secreted and transmembrane protein PRO301.
PN US20030082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 76
ID ADB14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 77
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US20030044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 78
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 79
ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 80
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 81
ID ADB13238 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 82
ID ABO43331 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 83
ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 84
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 85
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US20030077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1544; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 86
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082701-A1.
PD 01-MAY-2003.

RESULT 87
ID   ADA75212 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030073216-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 88
ID   ADA85290 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082695-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 89
ID   ADA84738 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082708-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 90
ID   ABO17514 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20030064367-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 91
ID   ADB29994 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030073214-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 92
ID   ADA80522 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082761-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 93
ID   ADA75764 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082703-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 94
ID   ADA46989 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030073210-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 95
ID   ADB25285 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077715-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match

RESULT 96
ID   ADA93461 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030077721-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 97
ID   ADB26811 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030092147-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 98
ID   ADB31098 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030093386-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 99
ID   ADA61026 standard; protein; 299 AA.
DE   Homo sapiens.
PN   US20030049817-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 100
ID   ADA24173 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077714-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 101
ID   ADA96502 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082690-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 102
ID   ADA81074 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082702-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 103
ID   ADA95950 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082759-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

RESULT 104
ID   ADB26259 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082760-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;
     Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
                                    Pred. No. 7.5e-105;

Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 105
ID ADB21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 6; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 106
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030687797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 107
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 108
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein, #25.
PN US20030082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 109
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 110
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030045622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 111
ID ADA41876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 112
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 113
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 114
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 115
ID ADA42726 standard; protein; 299 AA.
DE Human secreted and transmembrane protein, #25.
PN US20030054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 116
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 117
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 118
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 119
ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 120
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 121
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 122
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 100.0%; Score 1544; DB 7; Length 299;
Query Match 100.0%; Pred. No. 7.5e-105;

RESULT 123
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.

```
PN   US20030044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 124
ID   AB017575 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20030064923-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 125
ID   ADA66987 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 126
ID   ADB22848 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 127
ID   ADB23621 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 128
ID   ADA92343 standard; protein; 299 AA.
DE   Human secreted and transmembrane protein PRO301.
PN   US20030082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 129
ID   ADB15406 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 130
ID   ADB38658 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 131
ID   ADB38106 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087347-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 132
ID   ADB66578 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 133
ID   ADB89658 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 134
ID   ADB90390 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 135
ID   ADB77645 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030082764-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 136
ID   ADB39491 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082542-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 137
ID   ADB74781 standard; protein; 299 AA.
DE   Human secreted and transmembrane protein, #25.
PN   US20030082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 138
ID   ADB47114 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 139
ID   ADB67721 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 140
ID   ADB77326 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;
     Score 1544;  DB 7;  Length 299;

RESULT 141
ID   ADB34483 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077717-A1.
PD   24-APR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 142
ID   ADB35587 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 143
ID   ADB33931 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 144
ID   ADB35035 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 145
ID   ADB36139 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 146
ID   ADB46534 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 147
ID   ADC28427 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 148
ID   ADC39627 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003059828-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 149
ID   ADC40141 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 150
ID   ADC18969 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003036061-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match


     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 151
ID   ADC34265 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 152
ID   ADC29320 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003049676-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 153
ID   ADC28851 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 154
ID   ADC40736 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 155
ID   ADC19393 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 156
ID   ADC33841 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 157
ID   ADC12911 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 158
ID   ADC50407 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.

     Query Match    100.0%;  Pred. No. 7.5e-105;
     Best Local Similarity  100.0%;  Score 1544;  DB 7;  Length 299;
RESULT 159
ID   ADC71954 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 1544;  DB 7;  Length 299;
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Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 160
ID   ADC59933 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 161
ID   ADC52940 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 162
ID   ADC57294 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 163
ID   ADC60485 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 164
ID   ADC50960 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 165
ID   ADC65487 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 166
ID   ADC54585 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 167
ID   ADC53546 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 168
ID   ADC59069 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 169
ID   ADC55947 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 170
ID   ADC58517 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein Seq ID366.
PN   US20030087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 171
ID   ADC12363 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030082541-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 172
ID   ADD01191 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 173
ID   ADC90183 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 174
ID   ADC69602 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 175
ID   ADC48491 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 176
ID   ADD10020 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 177
ID   ADD04595 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;    Score 1544; DB 7; Length 299;
Best Local Similarity    100.0%;    Pred. No. 7.5e-105;

RESULT 178
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RESULT 179
ID   ADC80551 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030092103-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 180
ID   ADD11058 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 181
ID   ADD10343 standard; protein; 299 AA.
DE   Human secreted/transmembrane PRO polypeptide #27.
PN   US20030105011-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 182
ID   ADC47939 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 183
ID   ADD04918 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030104469-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 184
ID   ADC79999 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane PRO polypeptide #27.
PN   US20030087358-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 185
ID   ADD11303 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030105013-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 186
ID   ADD09468 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 187
ID   ADD03924 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030104381-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 188
ID   ADD03500 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 189
ID   ADD41181 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030203438-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 190
ID   ADD52320 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 191
ID   ADD53060 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030203437-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 192
ID   ADD53612 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane PRO polypeptide #27.
PN   US20030105012-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 193
ID   ADD37096 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 194
ID   ADD51768 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030203431-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 195
ID   ADD02567 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030203430-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 196
ID   ADD02001 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030203431-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
Best Local Similarity   100.0%; Score 1544; DB 7; Length 299;

RESULT 196
ID   ADD54183 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.

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PN  US20032034432-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 197
ID  ADD92500 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990030-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 198
ID  ADD91396 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990055-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 199
ID  ADE04010 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990057-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 200
ID  ADE32307 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20031994765-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 201
ID  ADE22239 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990056-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 202
ID  ADD79463 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032003428-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 203
ID  ADE41999 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031994772-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 204
ID  ADE17816 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990023-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 205
ID  ADD91948 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990053-A1.

PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 206
ID  ADE33411 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20031994767-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 207
ID  ADE33963 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20031994791-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 208
ID  ADD80015 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032074417-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 209
ID  ADD93052 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031994768-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 210
ID  ADE19472 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990025-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 211
ID  ADE34752 standard; protein; 299 AA.
DE  Human secreted/transmembrane protein, #25.
PN  US20032077583-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 212
ID  ADE18920 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990026-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 213
ID  ADE43116 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990033-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match  100.0%;  Score 1544;  DB 7;  Length 299;
    Best Local Similarity  100.0%;  Pred. No. 7.5e-105;
RESULT 214
ID  ADD95905 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990059-A1.
PD  23-OCT-2003.
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PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 215
ID   ADB22791 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 216
ID   ADD78909 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 217
ID   ADE32859 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 218
ID   ADE42551 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 219
ID   ADD80567 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 220
ID   ADD89595 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 221
ID   ADE40879 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 222
ID   ADE04678 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 223
ID   ADE92807 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 224
ID   ADG21516 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 225
ID   ADG23157 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 226
ID   ADF97492 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 227
ID   ADG80556 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 228
ID   ADG80004 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 229
ID   ADG63772 standard; protein; 299 AA.
DE   Human secreted/transmembrane polypeptide PRO301.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 230
ID   ADH62528 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 231
ID   ADH59235 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1544; DB 7; Length 299;
Best Local Similarity 100.0%;   Pred. No. 7.5e-105;
RESULT 232

ID   ADH55296 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207381-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 234
ID   ADH55848 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207379-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 235
ID   ADI38014 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein #25.
PN   US20030054352-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 236
ID   ADI64067 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207385-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 237
ID   ADI65016 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207386-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 238
ID   ADI63515 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207387-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 239
ID   ADH81929 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207388-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 240
ID   ADH81377 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207377-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 241
ID   AD826282 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030054349-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

ID   ADM82546 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207355-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 242
ID   ADN15945 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087353-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 243
ID   ADN16574 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087385-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 244
ID   ADN15393 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087356-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 245
ID   ADN14841 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087357-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 7; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 246
ID   ADC81103 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030092115-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 247
ID   ADE79197 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030135025-A1.
PD   17-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 248
ID   ADD76551 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030100087-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 249
ID   ADD87915 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030092113-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity   100.0%; Pred. No. 7.5e-105;

RESULT 250
ID   ADD86319 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.

PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 251
ID   ADE79621 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20031130489-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 252
ID   ADE75767 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032115721-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 253
ID   ADE73297 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20031229592-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 254
ID   ADE41304 standard; protein; 299 AA.
DE   Human secreted/transmembrane PRO polypeptide #27.
PN   US20031004597-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 255
ID   ADE22343 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030921108-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 256
ID   ADE23895 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030921110-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 257
ID   ADE24538 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030921111-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 258
ID   ADE87363 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032034439-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 259
ID   ADE89229 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031990062-A1.

PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 260
ID   ADE41186 standard; protein; 299 AA.
DE   Human secreted/transmembrane polypeptide PRO301.
PN   US20031045558-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 261
ID   ADE73832 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20031148370-A1.
PD   07-AUG-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 262
ID   ADE18368 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031994794-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 263
ID   ADE86777 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199054-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 264
ID   ADE99386 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199027-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 265
ID   ADE94697 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199061-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 266
ID   ADE91108 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199052-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 267
ID   ADE95249 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031990060-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1544;   DB 8;   Length 299;
     Best Local Similarity   100.0%;   Pred. No. 7.5e-105;
RESULT 268
ID   ADE93359 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031990060-A1.
PD   23-OCT-2003.

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PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 269
ID  ADF34940 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990029-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 270
ID  ADE98505 standard; protein; 299 AA.
DE  Human secreted/transmembrane protein; #25.
PN  US20032115569-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 271
ID  ADE92255 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20031990051-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 272
ID  ADE90556 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20031990063-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 273
ID  ADE91703 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20031990058-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 274
ID  ADE98932 standard; protein; 299 AA.
DE  Human secreted/transmembrane protein, #25.
PN  US20032115568-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 275
ID  ADG40402 standard; protein; 299 AA.
DE  Human secreted/transmembrane protein, #25.
PN  US20032253253-A1.
PD  04-DEC-2003.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 276
ID  ADF73796 standard; protein; 299 AA.
DE  Human secreted/transmembrane protein, #25.
PN  US20031803312-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;


RESULT 277
ID  ADG02282 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032073552-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 278
ID  ADG22068 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20032073560-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 279
ID  ADG20138 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032073576-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 280
ID  ADF99044 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032074422-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 281
ID  ADG24261 standard; protein; 299 AA.
DE  Novel human secreted and transmembrane protein PRO301.
PN  US20032074426-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 282
ID  ADF98615 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032080855-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 283
ID  ADG03446 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032073551-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 284
ID  ADG91167 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032073553-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 285
ID  ADG16752 standard; protein; 299 AA.
DE  Human PRO polypeptide #183.
PN  US20032073559-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
Query Match  100.0%;  Score 1544;  DB 8;  Length 299;
Best Local Similarity  100.0%;  Pred. No. 7.5e-105;

RESULT 286
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ID   ADG05211 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032073075-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 287
ID   ADG19478 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032074025-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 288
ID   ADF73372 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20031606051-A1.
PD   04-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 289
ID   ADG13315 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032073357-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 290
ID   ADG08372 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032074024-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 291
ID   ADG15542 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032073371-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 292
ID   ADF96940 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031219885-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 293
ID   ADG06125 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032073374-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 294
ID   ADG23709 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032073789-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 295
ID   ADG03998 standard; protein; 299 AA.

DE   Human PRO polypeptide #183.
PN   US20032073423-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 296
ID   ADG24899 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032074027-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 297
ID   ADG07196 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032073350-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 298
ID   ADG07748 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032073356-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 299
ID   ADG55243 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20031947778-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 300
ID   ADG60907 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032073390-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 301
ID   ADG62011 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032074028-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 302
ID   ADG92215 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20032073145-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 303
ID   ADG82212 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032073558-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1544; DB 8; Length 299;
     Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 304
ID   ADG57451 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.

PN US2003207362-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 305
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 306
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 307
ID ADG58555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 308
ID ADG70921 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207420-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 309
ID ADG92642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 310
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 311
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 312
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207146-Al.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 313
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 314
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-Al.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 315
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-Al.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 316
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 317
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 318
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 319
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-Al.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 320
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 321
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 8; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 322
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Left column

Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 323
ID   ADH28546 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030022331-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 324
ID   ADG54691 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207367-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 325
ID   ADG59731 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207369-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 326
ID   ADH20431 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040005553-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 327
ID   ADH43487 standard; protein; 299 AA.
DE   Human PRO polypeptide #27.
PN   US20030224984-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 328
ID   ADH07286 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040006211-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 329
ID   ADH59831 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030215904-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 330
ID   ADH06859 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040005665-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

Right column

RESULT 331
ID   ADI81155 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030207361-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 332
ID   ADI18601 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030152999-A1.
PD   14-AUG-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 333
ID   ADI65321 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030148419-A1.
PD   07-AUG-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 334
ID   ADI37584 standard; protein; 299 AA.
DE   Human secreted and transmembrane protein PRO301.
PN   US20030096340-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 335
ID   ADG09898 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20040009548-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 336
ID   ADH97380 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030190610-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 337
ID   ADI15369 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030207382-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 338
ID   ADG09246 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20040009547-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1544; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 7.5e-105;

RESULT 339
ID   ADI65748 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030148371-A1.
PA   (GETH) GENENTECH INC.

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PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 340
ID   ADI14701 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 341
ID   ADH60491 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040233331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 342
ID   ADI18296 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 343
ID   ADJ99548 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 344
ID   ADI08741 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 345
ID   ADI47176 standard; protein; 299 AA.
DE   Human JAM-1 protein sequence.
PN   WO2004003145-A2.
PD   08-JAN-2004.
PA   (NAST-) NASTECH PHARM CO INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 346
ID   ADM25082 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2004096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 347
ID   ADK40844 standard; protein; 299 AA.
DE   Human platelet F11 receptor #1.
PN   US5699688-B1.
PD   02-MAR-2004.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;

     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 348
ID   ADJ63577 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20040039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 349
ID   ADM29832 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 350
ID   ADL77818 standard; protein; 299 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN   US20040010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 351
ID   ADL77819 standard; protein; 299 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN   US20040010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 352
ID   ADJ77472 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 353
ID   ADK82832 standard; protein; 299 AA.
DE   Human PRO polypeptide #27.
PN   US20040049327-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 354
ID   ADJ65594 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 355
ID   ADL11332 standard; protein; 299 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3365.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             100.0%;  Score 1544;  DB 8;  Length 299;
     Best Local Similarity   100.0%;  Pred. No. 7.5e-105;
RESULT 356
ID   ADM27730 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
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RESULT 357
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADL26800 standard; protein; 299 AA.
DE Human JAM1 protein SEQ ID NO:54.
PN WO200402778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.

RESULT 358
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.

RESULT 359
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.

RESULT 360
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200403105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

RESULT 361
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADN05140 standard; protein; 299 AA.
DE Antipsoriatic protein sequence #749.
PN WO200402879-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.

RESULT 362
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004077064-A1.
PD 22-APR-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.

RESULT 363
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADQ95890 standard; protein; 299 AA.
DE T cell activation associated protein #34.
PN WO200405805-A2.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.

RESULT 364
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR11006 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US200413561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.

RESULT 365
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR17915 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US200414701-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.

PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERB/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

RESULT 366
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR27641 standard; protein; 299 AA.
DE Human F11 receptor protein seq 7.
PN WO200406327-A2.
PD 29-JUL-2004.
PA (GETH) GENENTECH INC.

RESULT 367
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADI95798 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307765S-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 368
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADI96350 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200320735-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

RESULT 369
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR46577 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, SEQ ID 8.
PN JP200424251-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

RESULT 370
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR46571 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP200424251-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

RESULT 371
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1544; DB 8; Length 299;
ID ADR46573 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP200424251-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match

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        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 372
ID    ADR46579 standard; protein; 299 AA.
DE    Human JAM-1, F11 receptor (F11R) transcript variant 5.
PN    JP2004242513-A.
PD    02-SEP-2004.
PA    (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 373
ID    ADP94260 standard; protein; 299 AA.
DE    Human PRO301 protein.
PN    AU2003259607-A1.
PD    27-NOV-2003.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 374
ID    ADS74554 standard; protein; 299 AA.
DE    Human secreted/transmembrane protein #25.
PN    US20041855531-A1.
PD    23-SEP-2004.
PA    (ASHK/) ASHKENAZI A.
PA    (BOTS/) BOTSTEIN D.
PA    (DESN/) DESNOYERS L.
PA    (EATO/) EATON D L.
PA    (FERR/) FERRARA N.
PA    (FILV/) FILVAROFF E.
PA    (FONG/) FONG S.
PA    (GAOW/) GAO W.
PA    (GERB/) GERBER H.
PA    (GERR/) GERRITSEN M E.
PA    (GODD/) GODDARD A.
PA    (GODO/) GODOWSKI P J.
PA    (GRIM/) GRIMALDI C J.
PA    (GURN/) GURNEY A L.
PA    (HILL/) HILLAN K J.
PA    (KLJA/) KLJAVIN I J.
PA    (MATH/) MATHER J P.
PA    (PANJ/) PAN J.
PA    (PAON/) PAONI N F.
PA    (ROYM/) ROY M A.
PA    (STEW/) STEWART T A.
PA    (TUMA/) TUMAS D.
PA    (WILL/) WILLIAMS P M.
PA    (WOOD/) WOOD W I.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 375
ID    ADS32302 standard; protein; 299 AA.
DE    Novel human secreted and transmembrane protein PRO301.
PN    US20042203125-A1.
PD    14-OCT-2004.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 376
ID    ADT03286 standard; protein; 299 AA.
DE    Human PRO polypeptide #183.
PN    US20042214269-A1.
PD    28-OCT-2004.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 377
ID    ADT03591 standard; protein; 299 AA.
DE    Human secreted/transmembrane protein, #25.
PN    US20031152922-A1.
PD    14-AUG-2003.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 378

ID    ADU06480 standard; protein; 299 AA.
DE    Novel bronchial cancer-associated human protein SeqID704.
PN    DE10316701-A1.
PD    04-NOV-2004.
PA    (HINZ/) HINZMANN B.
PA    (HERM/) HERMANN K.
PA    (CAST/) HEIDEN CASTANOS-VELEZ E.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 379
ID    ADU06355 standard; protein; 299 AA.
DE    Novel bronchial cancer-associated human protein SeqID579.
PN    DE10316701-A1.
PD    04-NOV-2004.
PA    (HINZ/) HINZMANN B.
PA    (HERM/) HERMANN K.
PA    (CAST/) HEIDEN CASTANOS-VELEZ E.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 380
ID    ADU66684 standard; protein; 299 AA.
DE    Human platelet F11 receptor protein, F11R-A.
PN    US20042235768-A1.
PD    25-NOV-2004.
PA    (KORN/) KORNECKI E.
PA    (SOBO/) SOBOCKA M B.
        Query Match    100.0%;   Score 1544;   DB 8;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 381
ID    ADW97860 standard; protein; 299 AA.
DE    Human junctional adhesion molecule-1 (JAM-1) protein.
PN    US20050025776-A1.
PD    03-FEB-2005.
PA    (WEBE/) WEBER C.
        Query Match    100.0%;   Score 1544;   DB 9;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 382
ID    ADZ03337 standard; protein; 299 AA.
DE    Human secreted/transmembrane PRO301 protein.
PN    US20050748337-A1.
PD    07-APR-2005.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 9;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 383
ID    AEA37829 standard; protein; 299 AA.
DE    Human secreted/transmembrane protein, #25.
PN    US20051112725-A1.
PD    26-MAY-2005.
PA    (GETH ) GENENTECH INC.
        Query Match    100.0%;   Score 1544;   DB 9;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 384
ID    AEA29245 standard; protein; 299 AA.
DE    Human junction adhesion molecule -1 as target for drug delivery method.
PN    US20050129679-A1.
PD    16-JUN-2005.
PA    (NAST-) NASTECH PHARM CO INC.
        Query Match    100.0%;   Score 1544;   DB 9;   Length 299;
        Best Local Similarity    100.0%;   Pred. No. 7.5e-105;
RESULT 385
ID    AEB14083 standard; protein; 299 AA.
DE    Cancer cell diagnosis method-related human protein - SEQ ID 366.
PN    US20050153396-A1.
PD    14-JUL-2005.
PA    (BAKE/) BAKER K P.
PA    (BERE/) BERESINI M.
PA    (DEFO/) DEFORGE L.
PA    (DESN/) DESNOYERS L.
PA    (FILV/) FILVAROFF E.
PA    (GAOW/) GAO W.
PA    (GERR/) GERRITSEN M E.
PA    (GODD/) GODDARD A.
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PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
    Query Match   100.0%; Score 1544; DB 9; Length 299;
    Best Local Similarity 100.0%; Pred. No. 7.5e-105;
RESULT 386
ID   ADE09073 standard; protein; 320 AA.
DE   Novel protein-related contig polypeptide sequence #139.
PN   WO200305154152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
    Query Match   100.0%; Score 1544; DB 7; Length 320;
    Best Local Similarity 100.0%; Pred. No. 8.1e-105;
RESULT 387
ID   ADU40591 standard; protein; 320 AA.
DE   Novel human polypeptide seq id 376.
PN   US200421952521-A1.
PD   04-NOV-2004.
PA   (TANG/) TANG Y T.
PA   (WANG/) WANG Z.
PA   (WENG/) WENG G.
PA   (BOYL/) BOYLE B J.
PA   (DRMA/) DRMANAC R T.
    Query Match   100.0%; Score 1544; DB 9; Length 320;
    Best Local Similarity 100.0%; Pred. No. 8.6e-105;
RESULT 388
ID   ADE08038 standard; protein; 336 AA.
DE   Novel protein (useful for identifying genetic disorders) #193.
PN   WO200305154152-A1.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
    Query Match   100.0%; Score 1544; DB 7; Length 336;
    Best Local Similarity 100.0%; Pred. No. 8.6e-105;
RESULT 389
ID   ADU40408 standard; protein; 336 AA.
DE   Novel human polypeptide seq id 193.
PN   US200421952521-A1.
PD   04-NOV-2004.
PA   (TANG/) TANG Y T.
PA   (WANG/) WANG Z.
PA   (WENG/) WENG G.
PA   (BOYL/) BOYLE B J.
PA   (DRMA/) DRMANAC R T.
    Query Match   100.0%; Score 1544; DB 9; Length 336;
    Best Local Similarity 100.0%; Pred. No. 8.1e-105;
RESULT 390
ID   AAY08071 standard; protein; 299 AA.
DE   Human PRO307 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1544; DB 9; Length 299;
    Best Local Similarity 100.0%; Pred. No. 8.6e-105;
RESULT 391
ID   ADC78439 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH) GENENTECH INC.
    Query Match   99.7%; Score 1540; DB 2; Length 299;
    Best Local Similarity 99.7%; Pred. No. 1.5e-104;
RESULT 392
ID   ADH80723 standard; protein; 300 AA.
DE   Human polypeptide #40.
PN   US20032232054-A1.
PD   18-DEC-2003.
PA   (TANG/) TANG Y T.
    Query Match   99.7%; Score 1539; DB 3; Length 299;
    Best Local Similarity 99.7%; Pred. No. 1.7e-104;

PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
    Query Match   98.5%; Score 1521.5; DB 8; Length 300;
    Best Local Similarity 99.0%; Pred. No. 3.3e-103;
RESULT 393
ID   ADH80722 standard; protein; 301 AA.
DE   Human polypeptide #39.
PN   US20032232054-A1.
PD   18-DEC-2003.
PA   (TANG/) TANG Y T.
PA   (LIUC/) LIU C.
PA   (ASUN/) ASUNDI V.
PA   (CHEN/) CHEN R.
PA   (QIAN/) QIAN X B.
PA   (WANG/) WANG Z W.
PA   (WEHR/) WEHRMAN T.
PA   (ZHAN/) ZHANG J.
PA   (ZHOU/) ZHOU P.
PA   (CAOY/) CAO Y.
PA   (DRMA/) DRMANAC R T.
    Query Match   97.5%; Score 1505; DB 8; Length 301;
    Best Local Similarity 98.3%; Pred. No. 5.4e-102;
RESULT 394
ID   ADJ67617 standard; protein; 351 AA.
DE   Human ovarian specific polypeptide SEQ ID NO:331.
PN   WO200401311-A2.
PD   12-FEB-2004.
PA   (DIAD-) DIADEXUS INC.
    Query Match   97.2%; Score 1500; DB 8; Length 351;
    Best Local Similarity 84.9%; Pred. No. 1.5e-101;
RESULT 395
ID   ADJ67616 standard; protein; 335 AA.
DE   Human ovarian specific polypeptide SEQ ID NO:330.
PN   WO200401311-A2.
PD   12-FEB-2004.
PA   (DIAD-) DIADEXUS INC.
    Query Match   91.4%; Score 1411; DB 8; Length 335;
    Best Local Similarity 97.1%; Pred. No. 4.6e-95;
RESULT 396
ID   AAU17996 standard; protein; 301 AA.
DE   Human immunoglobulin polypeptide SEQ ID No 141.
PN   WO200155315-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
    Query Match   90.4%; Score 1396.5; DB 4; Length 301;
    Best Local Similarity 92.0%; Pred. No. 4.7e-94;
RESULT 397
ID   ABB10232 standard; protein; 301 AA.
DE   Human cDNA SEQ ID NO: 540.
PN   WO200154474-A2.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
    Query Match   90.4%; Score 1396.5; DB 4; Length 301;
    Best Local Similarity 92.0%; Pred. No. 4.7e-94;
RESULT 398
ID   ABP66819 standard; protein; 301 AA.
DE   Human polypeptide SEQ ID NO 540.
PN   US20020090672-A1.
PD   11-JUL-2002.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
    Query Match   90.4%; Score 1396.5; DB 5; Length 301;
    Best Local Similarity 92.0%; Pred. No. 4.7e-94;
RESULT 399

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ID   ADB31620 standard; protein; 301 AA.
DE   Human novel protein SEQ ID NO 141.
PN   US20030177606-A1.
PD   24-APR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
       Query Match        90.4%;  Score 1396.5;  DB 7;  Length 301;
       Best Local Similarity   92.0%;  Pred. No. 4.7e-94;

RESULT 400
ID   ADR41522 standard; protein; 318 AA.
DE   Human CD-like molecule HKACIO3, SEQ ID NO:321.
PN   WO200226930-A2.
PD   04-APR-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
       Query Match        90.4%;  Score 1396.5;  DB 5;  Length 318;
       Best Local Similarity   92.0%;  Pred. No. 5e-94;

RESULT 401
ID   AAW61379 standard; protein; 298 AA.
DE   Human junctional adhesion molecule protein.
PN   WO9824897-A1.
PD   11-JUN-1998.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
       Query Match        89.5%;  Score 1382.5;  DB 2;  Length 298;
       Best Local Similarity   91.0%;  Pred. No. 4.9e-93;

RESULT 402
ID   AAY23328 standard; protein; 263 AA.
DE   An A33 related antigen sequence.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.
       Query Match        88.9%;  Score 1372;  DB 2;  Length 263;
       Best Local Similarity   100.0%;  Pred. No. 2.5e-92;

RESULT 403
ID   AAY08074 standard; protein; 263 AA.
DE   Human DNA40628 protein fragment #2.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
       Query Match        88.9%;  Score 1372;  DB 7;  Length 263;
       Best Local Similarity   100.0%;  Pred. No. 2.5e-92;

RESULT 404
ID   ADH62552 standard; protein; 263 AA.
DE   Human PRO301 protein fragment #2.
PN   US20031171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
       Query Match        88.9%;  Score 1372;  DB 7;  Length 263;
       Best Local Similarity   100.0%;  Pred. No. 2.5e-92;

RESULT 405
ID   AAY23326 standard; protein; 260 AA.
DE   An A33 related antigen sequence.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.
       Query Match        88.9%;  Score 1355;  DB 2;  Length 260;
       Best Local Similarity   100.0%;  Pred. No. 4.3e-91;

RESULT 406
ID   AAY08072 standard; protein; 260 AA.
DE   Human DNA40628 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
       Query Match        87.8%;  Score 1355;  DB 2;  Length 260;
       Best Local Similarity   100.0%;  Pred. No. 4.3e-91;

RESULT 407
ID   ADH62550 standard; protein; 260 AA.
DE   Human PRO301 protein fragment #1.
PN   US20031171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
       Query Match        87.8%;  Score 1355;  DB 7;  Length 260;
       Best Local Similarity   100.0%;  Pred. No. 4.3e-91;

RESULT 408
ID   ADQ95892 standard; protein; 259 AA.
DE   T cell activation associated protein #35.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
       Query Match        83.4%;  Score 1287;  DB 8;  Length 259;
       Best Local Similarity   86.3%;  Pred. No. 4.1e-86;

RESULT 409
ID   ADR46575 standard; protein; 259 AA.
DE   Human JAM-1, F11 receptor (F11R) transcript variant 3.
PN   JP2004242513-A.
PD   02-SEP-2004.
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
       Query Match        83.4%;  Score 1287;  DB 8;  Length 259;
       Best Local Similarity   86.3%;  Pred. No. 4.1e-86;

RESULT 410
ID   AAU14169 standard; protein; 259 AA.
DE   Human novel protein #40.
PN   WO200155437-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
       Query Match        83.0%;  Score 1281;  DB 4;  Length 259;
       Best Local Similarity   86.0%;  Pred. No. 1.1e-85;

RESULT 411
ID   ABU69130 standard; protein; 225 AA.
DE   Human NOVX polypeptide #5.
PN   WO20029504-A2.
PD   14-NOV-2002.
PA   (CURA-) CURAGEN CORP.
       Query Match        72.2%;  Score 1114;  DB 6;  Length 225;
       Best Local Similarity   75.3%;  Pred. No. 1.6e-73;

RESULT 412
ID   AD008263 standard; protein; 225 AA.
DE   Human NOVX polypeptide #5.
PN   US20040018594-A1.
PD   29-JAN-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CASM/) CASMAN S J.
PA   (CHAP/) CHAPOVAL A.
PA   (EDIN/) EDINGER S R.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUNT/) GUNTHER E.
PA   (GUOX/) GUO X S.
PA   (KEKU/) KEKUDA R.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LILL L.
PA   (LIUX/) LIU X.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLER C E.
PA   (MILL/) MILLET I.
PA   (PADI/) PADIGARU M.
PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (RIEG/) RIEGER D K.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
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PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
RESULT 413
    Query Match   72.2%; Score 1114;   DB 8; Length 225;
    Best Local Similarity   75.3%; Pred. No. 1.6e-73;
ID ADK46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN WO200242513-A.
PD 02-SEP-2004.
PA (DOKU/) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

RESULT 414
    Query Match   69.9%; Score 1079.5; DB 8; Length 300;
    Best Local Similarity   68.4%; Pred. No. 7.5e-71;
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

RESULT 415
    Query Match   69.5%; Score 1073.5; DB 2; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN WO9270998-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.

RESULT 416
    Query Match   69.5%; Score 1073.5; DB 7; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.

RESULT 417
    Query Match   69.5%; Score 1073.5; DB 8; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.

RESULT 418
    Query Match   69.5%; Score 1073.5; DB 8; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO200403105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

RESULT 419
    Query Match   69.5%; Score 1073.5; DB 8; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID ADU66693 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US200423768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.

RESULT 420
    Query Match   69.5%; Score 1073.5; DB 8; Length 300;
    Best Local Similarity   68.1%; Pred. No. 2.1e-70;
ID AAW74465 standard; protein; 205 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.

RESULT 421
    Query Match   67.5%; Score 1042.5; DB 2; Length 205;
    Best Local Similarity   98.5%; Pred. No. 2.5e-68;
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.

RESULT 422
    Query Match   67.2%; Score 1038;   DB 3; Length 280;
    Best Local Similarity   69.9%; Pred. No. 7.6e-68;
ID ADK40845 standard; protein; 193 AA.
DE Human platelet F11 receptor #2.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.

RESULT 423
    Query Match   58.9%; Score 910;   DB 8; Length 193;
    Best Local Similarity   97.2%; Pred. No. 1.1e-58;
ID ADU66685 standard; protein; 193 AA.
DE Human platelet F11 receptor protein, F1IR-B.
PN US200423768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.

RESULT 424
    Query Match   58.9%; Score 910;   DB 8; Length 193;
    Best Local Similarity   97.2%; Pred. No. 1.1e-58;
ID AAY75995 standard; protein; 193 AA.
DE Human skin cell protein, SEQ ID NO:173.
PN WO9958865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.

RESULT 425
    Query Match   37.3%; Score 576;   DB 3; Length 134;
    Best Local Similarity   100.0%; Pred. No. 2.1e-34;
ID AAB55934 standard; protein; 134 AA.
DE Skin cell protein, SEQ ID NO: 173.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.

RESULT 426
    Query Match   37.3%; Score 576;   DB 4; Length 134;
    Best Local Similarity   100.0%; Pred. No. 2.1e-34;
ID ABB72134 standard; protein; 134 AA.
DE Human protein isolated from skin cells SEQ ID NO: 173.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.

RESULT 427
    Query Match   37.3%; Score 576;   DB 5; Length 134;
    Best Local Similarity   100.0%; Pred. No. 2.1e-34;
ID AAU18030 standard; protein; 141 AA.
DE Human immunoglobulin polypeptide SEQ ID No 175.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

RESULT 428
    Query Match   34.0%; Score 525;   DB 4; Length 141;
    Best Local Similarity   100.0%; Pred. No. 1.2e-30;
ID AAM94741 standard; protein; 141 AA.
DE Human reproductive system related antigen SEQ ID NO: 3399.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

RESULT 429
    Query Match   34.0%; Score 525;   DB 4; Length 141;
    Best Local Similarity   100.0%; Pred. No. 1.2e-30;
ID ABB10228 standard; protein; 141 AA.
DE Human cDNA SEQ ID NO: 536.
PN WO200154474-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   34.0%; Score 525; DB 4; Length 141;
    Best Local Similarity 100.0%; Pred. No. 1.2e-30;

RESULT 430
ID AAU22763 standard; protein; 141 AA.
DE Human prostate cancer antigen, Seq ID No 282.
PN WO200153316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   34.0%; Score 525; DB 4; Length 141;
    Best Local Similarity 100.0%; Pred. No. 1.2e-30;

RESULT 431
ID ABP66815 standard; protein; 141 AA.
DE Human polypeptide SEQ ID NO 536.
PN US20020090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
    Query Match   34.0%; Score 525; DB 4; Length 141;
    Best Local Similarity 100.0%; Pred. No. 1.2e-30;

RESULT 432
ID ADB31654 standard; protein; 141 AA.
DE Human novel protein SEQ ID NO 175.
PN US20030077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   34.0%; Score 525; DB 7; Length 141;
    Best Local Similarity 100.0%; Pred. No. 1.2e-30;

RESULT 433
ID ADJ09336 standard; protein; 141 AA.
DE Human prostate cancer associated polypeptide SeqID282.
PN US20030054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   34.0%; Score 525; DB 7; Length 141;
    Best Local Similarity 100.0%; Pred. No. 1.2e-30;

RESULT 434
ID ADW97861 standard; protein; 88 AA.
DE Human JAM-1 protein active fragment.
PN US20050025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
    Query Match   30.0%; Score 463; DB 9; Length 88;
    Best Local Similarity 100.0%; Pred. No. 2.4e-26;

RESULT 435
ID AAW85457 standard; protein; 298 AA.
DE Secreted protein encoded by clone ct864_4.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
    Query Match   27.9%; Score 431; DB 2; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 436
ID AAU00512 standard; protein; 298 AA.
DE Human junctional adhesion protein (JAM2).
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
    Query Match   27.9%; Score 431; DB 4; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 437
ID ABP61801 standard; protein; 298 AA.
DE Human polypeptide SEQ ID NO 155.
PN US20020065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
    Query Match   27.9%; Score 431; DB 5; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 438
ID ABR58532 standard; protein; 298 AA.
DE Human JAM-3 protein sequence.
PN WO200403145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
    Query Match   27.9%; Score 431; DB 6; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 439
ID ADI47178 standard; protein; 298 AA.
DE Human vascular endothelial junction-associated molecule protein.
PN WO200325138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
    Query Match   27.9%; Score 431; DB 6; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 440
ID ADP56681 standard; protein; 298 AA.
DE Human junction adhesion molecule 2 (huJAM2) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
    Query Match   27.9%; Score 431; DB 8; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 441
ID ABM82288 standard; protein; 298 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO28687, SEQ:5880.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
    Query Match   27.9%; Score 431; DB 8; Length 298;
    Best Local Similarity 35.3%; Pred. No. 2.2e-23;

RESULT 442
ID AAW75220 standard; protein; 298 AA.
DE Human secreted protein encoded by gene 25 clone HTEEB42.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.8%; Score 429; DB 2; Length 298;
    Best Local Similarity 34.2%; Pred. No. 3.1e-23;

RESULT 443
ID AAE26983 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
PN US2002077287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREZ/) GREENE J M.
PA (FERR/) FERRIE A M.
    Query Match   27.8%; Score 429; DB 5; Length 298;
    Best Local Similarity 34.2%; Pred. No. 3.1e-23;

RESULT 444
ID AAE27121 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.

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PA   (KYAW/) KYAW H.
PA   (FISC/) FISCHER C L.
PA   (LIHH/) LI H.
PA   (SOPP/) SOPPET D R.
PA   (GENT/) GENTZ R L.
PA   (WEIY/) WEI Y.
PA   (MOOR/) MOORE P A.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 5;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 445
ID   ABR47926 standard; protein; 298 AA.
DE   Human secreted protein, SEQ ID 817.
PN   WO200295010-A2.
PD   28-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 6;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 446
ID   ABR00172 standard; protein; 298 AA.
DE   Human gene 162 encoded secreted protein HTEEB42, SEQ ID NO:461.
PN   WO200276488-A1.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 6;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 447
ID   ABU64994 standard; protein; 298 AA.
DE   Human secreted protein gene 25, protein.
PN   US2002172994-A1.
PD   21-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 6;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 448
ID   ADB91670 standard; protein; 298 AA.
DE   Human secreted protein #SEQ ID 616.
PN   WO2003004622-A2.
PD   16-JAN-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 7;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 449
ID   ADC74331 standard; protein; 298 AA.
DE   Human secreted protein - SEQ ID 964.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 7;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 450
ID   ADG89803 standard; protein; 298 AA.
DE   Human protein from secreted protein gene 25.
PN   US2003225009-A1.
PD   04-DEC-2003.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (LIYY/) LI Y.

PA   (ZENG/) ZENG Z.
PA   (KYAW/) KYAW H.
PA   (FISC/) FISCHER C L.
PA   (LIHH/) LI H.
PA   (SOPP/) SOPPET D R.
PA   (GENT/) GENTZ R L.
PA   (WEIY/) WEI Y.
PA   (MOOR/) MOORE P A.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
PA   (HAST/) HASTINGS G A.
     Query Match                27.8%;
     Best Local Similarity      34.2%;  Score 429;  DB 8;  Length 298;
                                Pred. No. 3.1e-23;
RESULT 451
ID   AAO16452 standard; protein; 298 AA.
DE   Human junctional adhesion molecule 2 (huJAM2).
PN   WO2003008541-A2.
PD   30-JAN-2003.
PA   (ELIL ) LILLY & CO ELI.
     Query Match
     Best Local Similarity      27.7%;  Score 428;  DB 6;  Length 298;
                                Pred. No. 3.6e-23;
RESULT 452
ID   AAO16453 standard; protein; 310 AA.
DE   Human junctional adhesion molecule 3 (huJAM3).
PN   WO2003008541-A2.
PD   30-JAN-2003.
PA   (ELIL ) LILLY & CO ELI.
     Query Match
     Best Local Similarity      38.3%;  Score 427;  DB 6;  Length 298;
                                Pred. No. 4.5e-23;
RESULT 453
ID   AAY96735 standard; protein; 310 AA.
DE   Human PRO1868, an A33 antigen homologue.
PN   WO2000053758-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity      27.5%;  Score 424;  DB 3;  Length 310;
                                Pred. No. 7.5e-23;
RESULT 454
ID   AAB33457 standard; protein; 310 AA.
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN   WO2000053758-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity      32.8%;  Score 424;  DB 3;  Length 310;
                                Pred. No. 7.5e-23;
RESULT 455
ID   AAB27276 standard; protein; 310 AA.
DE   Human confluency regulated adhesion molecule 1 #2.
PN   WO200053749-A2.
PD   14-SEP-2000.
PA   (RMFD-) RMF DICTAGENE SA.
     Query Match
     Best Local Similarity      27.5%;  Score 424;  DB 3;  Length 310;
                                Pred. No. 7.5e-23;
RESULT 456
ID   AAB80272 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity      32.8%;  Score 424;  DB 4;  Length 310;
                                Pred. No. 7.5e-23;
RESULT 457
ID   AAM93905 standard; protein; 310 AA.
DE   Human polypeptide, SEQ ID NO: 4051.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
     Query Match
     Best Local Similarity      27.5%;  Score 424;  DB 4;  Length 310;
                                Pred. No. 7.5e-23;
RESULT 458
ID   AAM93323 standard; protein; 310 AA.
DE   Human polypeptide, SEQ ID NO: 2845.
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PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
    Query Match   27.5%; Score 424; DB 4; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 459
ID AAU12440 standard; protein; 310 AA.
DE Human PRO1868 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 4; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 460
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 4; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 461
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 4; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 462
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 4; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 463
ID ABG92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US20020098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 464
ID ABG91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US20020098505-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 465
ID ABB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200206690-A2.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 466
ID ABG65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 467
ID ABG65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PN WO200177137-A1.

PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 468
ID ABG65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 469
ID ABG31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US20020098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 470
ID ABB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
    Query Match   27.5%; Score 424; DB 5; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 471
ID ABU71650 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US20020146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 6; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 472
ID ABU72377 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20020182618-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 6; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 473
ID ABU80867 standard; protein; 310 AA.
DE Human secreted and transmembrane polypeptide PRO1868.
PN US20020192668-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 6; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 474
ID ABO17884 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

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RESULT 475
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU71505 standard; protein; 310 AA.
DE   Human PRO polypeptide #61.
PN   US20021922659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.

RESULT 476
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ADA57610 standard; protein; 310 AA.
DE   Human secreted protein #592.
PN   WO200210294-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 477
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ADA57611 standard; protein; 310 AA.
DE   Human secreted protein #592.
PN   WO200210294-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 478
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ADA57309 standard; protein; 310 AA.
DE   Human secreted protein #592.
PN   WO200210294-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 479
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABP71277 standard; protein; 310 AA.
DE   Human junctional adhesion molecule 3 (JAM3).
PN   WO200306673-A2.
PD   23-JAN-2003.
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.

RESULT 480
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU81138 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 481
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU71951 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein PRO1868.
PN   US20030003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 482
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABO01834 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20021976571-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.

RESULT 483
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU66838 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity


RESULT 484
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU54407 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein PRO1868.
PN   US20021232240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.

RESULT 485
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABO47422 standard; protein; 310 AA.
DE   Human secreted/transmembrane polypeptide PRO1868.
PN   US20030044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 486
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABG73314 standard; protein; 310 AA.
DE   Human PRO1868 polypeptide.
PN   US20021646646-A1.
PD   07-NOV-2002.
PA   (GETH ) GENENTECH INC.

RESULT 487
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU59919 standard; protein; 310 AA.
DE   Novel secreted and transmembrane protein PRO1868.
PN   US20031017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 488
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABO25109 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein (PRO) #269.
PN   US20030036179-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.

RESULT 489
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU64559 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #63.
PN   US20021160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.

RESULT 490
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABU67405 standard; protein; 310 AA.
DE   Human secreted protein PRO1868.
PN   US20030023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 491
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID   ABO14925 standard; protein; 310 AA.
DE   Human secreted/ transmembrane polypeptide PRO1868.
PN   US20030036060-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 492
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;  Pred.
ID   ABU60813 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US20021603921-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match            27.5%;  Score 424;  DB 6;  Length 310;
  Best Local Similarity  32.8%;
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RESULT 493
ID   AB067114 standard; protein; 310 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN   US20030322155-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 494
ID   ABU81236 standard; protein; 310 AA.
DE   Human PRO1917polypeptide.
PN   US20030320060-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 495
ID   ABU69682 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030317463-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 496
ID   AB014864 standard; protein; 310 AA.
DE   Human secreted / transmembrane polypeptide PRO1868.
PN   US20030271143-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 497
ID   ADA46057 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868+H30.
PN   US20030322328-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 498
ID   ADA76488 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030073212-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 499
ID   ADB29627 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030092002-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 500
ID   ADA19138 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030054517-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 501
ID   ADA61761 standard; protein; 310 AA.
DE   Homo sapiens.
PN   US20030049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 502
ID   ADB19546 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 503
ID   ADB28087 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 504
ID   ADA86566 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 505
ID   ADB16130 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 506
ID   ADA47916 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030073215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 507
ID   ADA18484 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein PRO1868.
PN   US20030039971-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 508
ID   ABO32816 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030045693-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 509
ID   ADA67711 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 510
ID   ADB30718 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 511
ID   ADA86014 standard; protein; 310 AA.

DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082693-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 512
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA97226 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082705-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 513
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA79530 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082763-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 514
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA87669 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030087345-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 515
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB16871 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087349-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 516
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ABO34876 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030044793-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
RESULT 517
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA16459 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030049621-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
RESULT 518
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA91963 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082694-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 519
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB15026 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087351-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 520
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB18987 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.

PN   US20030073211-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
RESULT 521
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA94202 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030077722-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
RESULT 522
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB20098 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082691-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 523
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB13410 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082710-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 524
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ABO43417 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030044945-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
RESULT 525
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA74664 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068798-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
RESULT 526
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA42604 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030054401-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
RESULT 527
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADB24897 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US20030077713-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
RESULT 528
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA82421 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082701-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 529
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
Query Match   32.8%;   Pred. No. 7.5e-23;
ID   ADA75384 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030073216-A1.

PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 530
ID   ADA85462 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 531
ID   ADA84910 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 532
ID   AB017554 standard; protein; 310 AA.
DE   Human PRO polypeptide #61.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 533
ID   ADB30166 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 534
ID   ADA80694 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 535
ID   ADA75936 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 536
ID   ADA47161 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 537
ID   ADB25457 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 538
ID   ADA93633 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003077721-A1.
PD   24-APR-2003.

PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 539
ID   ADB26983 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 540
ID   ADB31270 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 541
ID   ABU62957 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   US2003054447-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 542
ID   ADA61198 standard; protein; 310 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 543
ID   ADB24345 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 544
ID   ADA96674 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 545
ID   ADA81246 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 546
ID   ADA96122 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 6; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;
RESULT 547
ID   ADB26431 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 548
ID ADB21916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 549
ID ADA77695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030687797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 6;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 550
ID ADB18435 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 551
ID ADA87118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein #65.
PN US20030082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 552
ID ADA16883 standard; protein; 310 AA.
DE Human secreted and transmembrane protein, #65.
PN US20030039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 553
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 554
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 555
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 556
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match

Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
RESULT 557
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 558
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 559
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 560
ID ADA29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 561
ID AB001894 standard; protein; 310 AA.
DE Human secreted and transmembrane protein PRO1868.
PN US20030027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 562
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 563
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 564
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   Score 424;   DB 7;   Length 310;
                         32.8%;   Pred. No. 7.5e-23;
RESULT 565
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030222239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 566

ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
PD 08-MAY-2003.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 567
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 01-APR-2003.
PA (GETH) GENENTECH INC.
PD 03-APR-2003.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 568
ID ADA67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
PD 24-APR-2003.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 569
ID ADB23020 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 570
ID ADB23793 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 571
ID ADA92515 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 572
ID ADB15578 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 573
ID ADB38830 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 574
ID ADB38278 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 575
ID ADB66750 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.

PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 576
ID ADB89830 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 577
ID ADB90562 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 578
ID ADB77948 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 579
ID ADB39663 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein, #65.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 580
ID ADB75084 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 581
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 582
ID ADB86893 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 583
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 27.5%; Score 424; DB 7; Length 310;
Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 584
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077717-A1.

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PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADB35759 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 585
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADB34103 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 586
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADB35207 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 587
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADB36311 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 588
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADB46706 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
RESULT 589
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC28731 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 590
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC39931 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003059828-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 591
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC40445 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 592
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC19269 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003036061-A1.
PD   20-FEB-2003.


PA   (GETH ) GENENTECH INC.
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC34569 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
RESULT 594
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC29624 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003049676-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 595
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC29155 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 596
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC41040 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 597
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC19697 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 598
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC34145 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 599
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC13215 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 600
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   AAE38826 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   US2003077657-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 601
     Query Match     27.5%;    Score 424;   DB 7;
     Best Local Similarity  32.8%;   Pred. No. 7.5e-23;   Length 310;

ID   ADC50579 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 603
ID   ADC72126 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 604
ID   ADC60105 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 605
ID   ADC53112 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 606
ID   ADC57466 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 607
ID   ADC60657 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 608
ID   ADC51132 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 609
ID   ADC65659 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 610
ID   ADC54757 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 611
ID   ADC53718 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 612
ID   ADC59241 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 613
ID   ADC56119 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 614
ID   ADC56689 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 615
ID   ADC12667 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030082541-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 616
ID   ADC74383 standard; protein; 310 AA.
DE   Human secreted protein - SEQ ID 1016.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 617
ID   ADC74606 standard; protein; 310 AA.
DE   Human secreted protein - SEQ ID 1229.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 618
ID   ADC74607 standard; protein; 310 AA.
DE   Human secreted protein - SEQ ID 1240.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 619
ID   ADD03363 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
RESULT 620
ID   ADC90355 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID538.
PN   US20030087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match      27.5%;  Score 424;  DB 7;  Length 310;
Best Local Similarity  32.8%;
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RESULT 621
ID   ADC69774 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 622
ID   ADC48663 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 623
ID   ADD10192 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 624
ID   ADD04767 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 625
ID   ADC80723 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 626
ID   ADD11230 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 627
ID   ADD10551 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO polypeptide #131.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 628
ID   ADC48111 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 629
ID   ADD05222 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;

RESULT 630

RESULT 631
ID   ADC80171 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 632
ID   ADD11511 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO polypeptide #131.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 633
ID   ADD09640 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 634
ID   ADD04228 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 635
ID   ADD03804 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein, #65.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 636
ID   ADD41353 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 637
ID   ADD52492 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 638
ID   ADD53232 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;
Pred. No. 7.5e-23;

RESULT 639
ID   ADD53784 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%;
Best Local Similarity   32.8%; Score 424; DB 7; Length 310;

RESULT 639
ID   ADD37304 standard; protein; 310 AA.

DE Human secreted/transmembrane PRO polypeptide #131.
PD US2003105012-A1.
PA 05-JUN-2003.
PN (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 640
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20031944779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 641
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20032043l-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 642
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO20029056-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 643
ID ADD38009 standard; protein; 192.
DE Human secreted protein #192.
PN WO20029056-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 644
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO20029056-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 645
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200320430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 646
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US200320432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 647
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319930-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 648
ID ADD51568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

PN US200319955-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 649
ID ADE04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 650
ID ADE32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US200319765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 651
ID ADE22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319956-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 652
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200320342-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 653
ID ADE42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319472-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 654
ID ADE17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319923-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 655
ID ADD91120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US200319767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 656
ID ADE33583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US200319053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   27.5%; Score 424; DB 7; Length 310;
    Best Local Similarity 32.8%; Pred. No. 7.5e-23;

RESULT 657
ID ADE34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US200319479l-A1.

PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Length 310;

RESULT 658
ID   ADD80187 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 659
ID   ADD99224 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 660
ID   ADB19644 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 661
ID   ADE35056 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003077583-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 662
ID   ADE19092 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 663
ID   ADE43288 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 664
ID   ADD96077 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 665
ID   ADE22963 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 666
ID   ADD79081 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003203429-A1.
PD   30-OCT-2003.

PA   (GETH) GENENTECH INC.
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 667
ID   ADE33031 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 668
ID   ADB42723 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 669
ID   ADD80739 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 670
ID   ADD89767 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 671
ID   ADE41051 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 672
ID   ADE04850 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 673
ID   ADE92979 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 674
ID   ADG21688 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%;
     Best Local Similarity   32.8%; Score 424; DB 7; Pred. No. 7.5e-23; Length 310;

RESULT 675
ID   ADG23329 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 676
ID   ADF97664 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 677
ID   ADG80728 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 678
ID   ADG80176 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 679
ID   ADH62558 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 680
ID   ADH59539 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 681
ID   ADH55468 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein #65.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 682
ID   ADH56020 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 683
ID   ADI38318 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 684

ID   ADI64239 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 685
ID   ADI65188 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 686
ID   ADI63687 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 687
ID   ADH82101 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 688
ID   ADH81549 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 689
ID   ADH82718 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   US2003170864-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 690
ID   ADJ58518 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 691
ID   ADJ26586 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 692
ID   ADN16117 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   27.5%;   32.8%;   Score 424;   DB 7;   Pred. No. 7.5e-23;   Length 310;

RESULT 693
ID   ADN16746 standard; protein; 310 AA.

DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087395-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 694
ID   ADN15565 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 7; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 695
ID   ADN15013 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 7; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 696
ID   ADC81275 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 7; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 697
ID   ADE79501 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 698
ID   ADD76723 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 699
ID   ADD88087 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 700
ID   ADD86491 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 701
ID   ADE79925 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 702
ID   ADE75939 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.

PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 703
ID   ADE73601 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 704
ID   ADE41512 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO polypeptide #131.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 705
ID   ADE23515 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 706
ID   ADE24067 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 707
ID   ADE24710 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 708
ID   ADD87535 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 709
ID   ADD89401 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 710
ID   ADE74136 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 711
ID   ADE18540 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194794-A1.

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PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 712
ID  ADB88849 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319054-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 713
ID  ADE99690 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200321576-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 714
ID  ADE94869 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319927-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 715
ID  ADE91280 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319961-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 716
ID  ADE95421 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319052-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 717
ID  ADE93531 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319060-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 718
ID  ADF35112 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319029-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 719
ID  ADE98809 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200321569-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 720
ID  ADE92427 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US200319051-A1.
PD  23-OCT-2003.

PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 721
ID  ADE90728 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200319063-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 722
ID  ADE91875 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US200319058-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 723
ID  ADE99236 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200321568-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 724
ID  ADG40706 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200322253-A1.
PD  04-DEC-2003.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD P A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 725
ID  ADF74100 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200318312-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 726
ID  ADG02454 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200320752-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 727
ID  ADG22240 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US200320736-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
RESULT 728
ID  ADG20310 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US200320376-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      27.5%;    Score 424;   DB 8;   Length 310;
    Best Local Similarity    32.8%;    Pred. No. 7.5e-23;
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RESULT 729
ID   ADF99216 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 730
ID   ADG24433 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 731
ID   ADF98787 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 732
ID   ADF03618 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 733
ID   ADF99339 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 734
ID   ADG16924 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 735
ID   ADG05383 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 736
ID   ADG19650 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 737
ID   ADF73676 standard; protein; 310 AA.

RESULT 738

RESULT 738
ID   ADG13487 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 739
ID   ADG08544 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 740
ID   ADG15714 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 741
ID   ADF97112 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 742
ID   ADG06297 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 743
ID   ADG23881 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 744
ID   ADG04170 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 745
ID   ADG25071 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 746
ID   ADG07368 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   27.5%; Score 424; DB 8; Length 310;
     Best Local Similarity   32.8%; Pred. No. 7.5e-23;

RESULT 747
ID   ADG07920 standard; protein; 310 AA.

DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 748
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG55415 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

RESULT 749
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG61079 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 750
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG62183 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 751
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG92519 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003207145-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.

RESULT 752
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG82384 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 753
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG57623 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 754
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG57071 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 755
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG55967 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 756
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG58727 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.

PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 757
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG71093 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 758
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG92946 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003207146-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.

RESULT 759
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG58175 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 760
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG53759 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 761
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG71645 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 762
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG81832 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.

RESULT 763
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADH30794 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 764
Query Match   27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADH12161 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207414-A1.
PD   06-NOV-2003.

RESULT 765
Best Local Similarity   32.8%;   Pred. No. 7.5e-23;
ID   ADG52583 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.

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PA   (GETH ) GENENTECH INC.
ID   ADG54311 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 767
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADG81280 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
RESULT 768
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADG56519 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 769
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH12785 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 770
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADG61631 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 771
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH28718 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
RESULT 772
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADG54863 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 773
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADG59903 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 774
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH20735 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
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RESULT 775
Query Match             32.8%;   Score 424;   DB 8;   Length 310;
Best Local Similarity   27.5%;   Pred. No. 7.5e-23;
ID   ADH43695 standard; protein; 310 AA.
DE   Human PRO polypeptide #131.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
PA   (DESN/) DESNOYERS L.
PD   08-JAN-2004.
RESULT 776
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH07590 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 777
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH60135 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2004005665-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
RESULT 778
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADH07163 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
RESULT 779
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADI81327 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 780
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADI18905 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003152999-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
RESULT 781
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADI65625 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003148419-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
RESULT 782
Best Local Similarity   27.5%;   Score 424;   DB 8;   Length 310;
Query Match             32.8%;   Pred. No. 7.5e-23;
ID   ADI37884 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
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PN  US20030096340-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 783
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADG10070 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US20040095548-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.

RESULT 784
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADH97684 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein; #65.
PN  US20031907610-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.

RESULT 785
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI15541 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US20030207382-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.

RESULT 786
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADG09418 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US20040009547-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.

RESULT 787
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI66052 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20030148371-A1.
PD  07-AUG-2003.
PA  (GETH ) GENENTECH INC.

RESULT 788
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI10341 standard; protein; 310 AA.
DE  Human PRO1868 protein from DNA77624-2515 clone.
PN  US20030228664-A1.
PD  11-DEC-2003.
PA  (GETH ) GENENTECH INC.

RESULT 789
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI14873 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein, #65.
PN  US20030207383-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.

RESULT 790
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADH60795 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20040023331-A1.
PD  05-FEB-2004.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.

RESULT 791
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI18468 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US20030207349-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.

RESULT 792
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADJ99852 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20031872388-A1.
PD  02-OCT-2003.
PA  (GETH ) GENENTECH INC.

RESULT 793
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADL09045 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20031863358-A1.
PD  02-OCT-2003.
PA  (GETH ) GENENTECH INC.

RESULT 794
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADI71177 standard; protein; 310 AA.
DE  Human JAM-2 protein sequence.
PN  WO20040003145-A2.
PD  08-JAN-2004.
PA  (NAST-) NASTECH PHARM CO INC.

RESULT 795
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADM25386 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20030096233-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.

RESULT 796
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADJ63749 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US20040003164-A1.
PD  26-FEB-2004.
PA  (GETH ) GENENTECH INC.

RESULT 797
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADM30136 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US20031906211-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.

RESULT 798
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADL78563 standard; protein; 310 AA.
DE  Albumin fusion protein related therapeutic protein X, SEQ ID No 2045.
PN  US20040010134-A1.
PD  15-JAN-2004.
PA  (HASE/) HASELTINE W A.
PA  (ROSE/) ROSEN C A.

RESULT 799
    Query Match            27.5%;  Score 424;  DB 8;  Length 310;
    Best Local Similarity  32.8%;  Pred. No. 7.5e-23;
ID  ADL78564 standard; protein; 310 AA.
DE  Albumin fusion protein related therapeutic protein X, SEQ ID No 2046.
PN  US20040010134-A1.
PD  15-JAN-2004.
PA  (ROSE/) ROSEN C A.
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PA   (HASE/) HASELTINE W A.
Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 800
ID   ADL789565 standard; protein; 310 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 2047.
PN   US20040101134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 801
PA   (GETH) GENENTECH INC.
ID   ADJ77644 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20040038336-A1.
PD   26-FEB-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 802
PA   (GETH) GENENTECH INC.
ID   ADK83040 standard; protein; 310 AA.
DE   Human PRO polypeptide #131.
PN   US20040043927-A1.
PD   04-MAR-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 803
PA   (GETH) GENENTECH INC.
ID   ADJ65766 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20040038335-A1.
PD   26-FEB-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 804
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
ID   ADL30812 standard; protein; 310 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 2845.
PN   EP1396543-A2.
PD   10-MAR-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 805
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
ID   ADL32018 standard; protein; 310 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 4051.
PN   EP1396543-A2.
PD   10-MAR-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 806
PA   (GETH) GENENTECH INC.
ID   ADM27902 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20040048333-A1.
PD   11-MAR-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 807
PA   (GETH) GENENTECH INC.
ID   ADM42626 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20040058424-A1.
PD   25-MAR-2004.

Query Match   27.5%; Score 424; DB 8;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 808
ID   AD06458 standard; protein; 310 AA.
DE   Human PRO polypeptide #60.
PN   US6686451-B1.
PD   03-FEB-2004.

PA   (GETH) GENENTECH INC.
Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 809
ID   ADN35310 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 810
ID   ADM28488 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20040077064-A1.
PD   22-APR-2004.
PA   (CURA-) CURAGEN CORP.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 811
ID   ADP69027 standard; protein; 310 AA.
DE   Human NOV2b protein SEQ ID NO:22.
PN   WO2004055158-A2.
PD   01-JUL-2004.
PA   (CURA-) CURAGEN CORP.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 812
ID   ADP69025 standard; protein; 310 AA.
DE   Human NOV2a protein SEQ ID NO:20.
PN   WO2004055158-A2.
PD   01-JUL-2004.
PA   (CURA-) CURAGEN CORP.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 813
ID   ADP69033 standard; protein; 310 AA.
DE   Human NOV2e protein SEQ ID NO:28.
PN   WO2004055158-A2.
PD   01-JUL-2004.
PA   (CURA-) CURAGEN CORP.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 814
ID   ADP69035 standard; protein; 310 AA.
DE   Human NOV2f protein SEQ ID NO:30.
PN   WO2004055158-A2.
PD   01-JUL-2004.
PA   (CURA-) CURAGEN CORP.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 815
ID   ADR11310 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20040137561-A1.
PD   15-JUL-2004.
PA   (GETH) GENENTECH INC.

Query Match   27.5%; Score 424; DB 8; Length 310;
Best Local Similarity   32.8%; Pred. No. 7.5e-23;
RESULT 816
ID   ADR18219 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20040147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.

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PA   (GERR/)   GERRITSEN M E.
PA   (GODD/)   GODDARD A.
PA   (GODO/)   GODOWSKI P. J.
PA   (GRIM/)   GRIMALDI C J.
PA   (GURN/)   GURNEY A L.
PA   (HILL/)   HILLAN K J.
PA   (KLJA/)   KLJAVIN I J.
PA   (MATH/)   MATHER J P.
PA   (PANJ/)   PAN J.
PA   (PAON/)   PAONI N F.
PA   (ROYM/)   ROY M A.
PA   (STEW/)   STEWART T A.
PA   (TUMA/)   TUMAS D.
PA   (WILL/)   WILLIAMS P M.
PA   (WOOD/)   WOOD W I.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 817
ID   ADI95970 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 818
ID   ADI96522 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 819
ID   ADS74858 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein #65.
PN   US2004185531-A1.
PD   23-SEP-2004.
PA   (ASHK/)   ASHKENAZI A.
PA   (BOTS/)   BOTSTEIN D.
PA   (DESN/)   DESNOYERS L.
PA   (EATO/)   EATON D L.
PA   (FERR/)   FERRARA N.
PA   (FILV/)   FILVAROFF E.
PA   (FONG/)   FONG S.
PA   (GAOW/)   GAO W.
PA   (GERB/)   GERBER H.
PA   (GERR/)   GERRITSEN M E.
PA   (GODD/)   GODDARD A.
PA   (GODO/)   GODOWSKI P J.
PA   (GRIM/)   GRIMALDI C J.
PA   (GURN/)   GURNEY A L.
PA   (HILL/)   HILLAN K J.
PA   (KLJA/)   KLJAVIN I J.
PA   (MATH/)   MATHER J P.
PA   (PANJ/)   PAN J.
PA   (PAON/)   PAONI N F.
PA   (ROYM/)   ROY M A.
PA   (STEW/)   STEWART T A.
PA   (TUMA/)   TUMAS D.
PA   (WILL/)   WILLIAMS P M.
PA   (WOOD/)   WOOD W I.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 820
ID   ADS32474 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2004203125-A1.
PD   14-OCT-2004.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 821


ID   ADT03458 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2004214269-A1.
PD   28-OCT-2004.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 822
ID   ADT03895 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003152922-A1.
PD   14-AUG-2003.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 823
ID   ADZ03509 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein PRO1868 protein.
PN   US2005074837-A1.
PD   07-APR-2005.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 8;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 824
ID   ABA38133 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH )   GENENTECH INC.
Query Match          27.5%;   Score 424;   DB 9;   Length 310;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 825
ID   AEB14255 standard; protein; 310 AA.
DE   Cancer cell diagnosis method-related human protein - SEQ ID 538.
PN   US2005153396-A1.
PD   14-JUL-2005.
PA   (BAKE/)   BAKER K P.
PA   (BERE/)   BERESINI M.
PA   (DEFO/)   DEFORGE L.
PA   (DESN/)   DESNOYERS L.
PA   (FILV/)   FILVAROFF E.
PA   (GAOW/)   GAO W.
PA   (GERR/)   GERRITSEN M E.
PA   (GODD/)   GODDARD A.
PA   (GODO/)   GODOWSKI P J.
PA   (GURN/)   GURNEY A L.
PA   (SHER/)   SHERWOOD S.
PA   (SMIT/)   SMITH V.
PA   (STEW/)   STEWART T A.
PA   (TUMA/)   TUMAS D.
PA   (WATA/)   WATANABE C K.
PA   (WOOD/)   WOOD W I.
PA   (ZHAN/)   ZHANG Z.
Query Match          27.5%;   Score 424;   DB 9;   Length 311;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 826
ID   AAB38383 standard; protein; 311 AA.
DE   Human secreted protein encoded by gene 13 clone HAPSA79.
PN   WO200061623-A1.
PD   19-OCT-2000.
PA   (HUMA-)   HUMAN GENOME SCI INC.
Query Match          27.5%;   Score 424;   DB 3;   Length 311;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 827
ID   AAB38384 standard; protein; 311 AA.
DE   Human secreted protein encoded by gene 13 clone HAPSA79.
PN   WO200061623-A1.
PD   19-OCT-2000.
PA   (HUMA-)   HUMAN GENOME SCI INC.
Query Match          27.5%;   Score 424;   DB 3;   Length 311;
Best Local Similarity  32.8%;   Pred. No. 7.5e-23;
RESULT 828
ID   AAB38333 standard; protein; 311 AA.
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(RESULT 828, continued from previous page)
DE   Human secreted protein encoded by gene 13 clone HAPSA79.
PD   19-OCT-2000.
PN   WO20061623-A1.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 829
  Best Local Similarity 32.8%;  Score 424;  DB 5;  Length 329;
  Query Match 27.5%;  Pred. No. 8.3e-23;
ID   ABP41902 standard; protein; 329 AA.
DE   Human ovarian antigen HISAF60, SEQ ID NO:3034.
PN   WO20200677-A1.
PD   03-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 830
  Best Local Similarity 32.8%;  Score 424;  DB 4;  Length 339;
  Query Match 27.5%;  Pred. No. 8.3e-23;
ID   AAB80431 standard; peptide; 339 AA.
DE   Gene #13 associated peptide #1.
PN   WO200107459-A1.
PD   01-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 831
  Best Local Similarity 32.8%;  Score 424;  DB 3;  Length 310;
  Query Match 27.5%;  Pred. No. 8.3e-23;
ID   AAY96294 standard; protein; 310 AA.
DE   Human IGFAM-6 immunoglobulin.
PN   WO20029583-A2.
PD   25-MAY-2000.
PA   (INCY-) INCYTE PHARM INC.

RESULT 832
  Best Local Similarity 32.8%;  Score 419;  DB 8;  Length 310;
  Query Match 27.1%;  Pred. No. 1.7e-22;
ID   ADP56683 standard; protein; 310 AA.
DE   Human junction adhesion molecule 3 (huJAM3) full-length protein.
PN   WO20040053058-A2.
PD   24-JUN-2004.
PA   (ELIL ) LILLY & CO ELI.

RESULT 833
  Best Local Similarity 32.8%;  Score 419;  DB 4;  Length 303;
  Query Match 27.1%;  Pred. No. 1.7e-22;
ID   AAM23693 standard; protein; 303 AA.
DE   Human EST encoded protein SEQ ID NO: 1218.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.

RESULT 834
  Best Local Similarity 34.4%;  Score 415.5;  DB 4;  Length 310;
  Query Match 26.9%;  Pred. No. 3.4e-22;
ID   AAB27278 standard; protein; 310 AA.
DE   Murine confluency regulated adhesion molecule 1.
PN   WO200053749-A2.
PD   14-SEP-2000.
PA   (RMFD-) RMF DICTAGENE SA.

RESULT 835
  Best Local Similarity 33.8%;  Score 415;  DB 3;  Length 310;
  Query Match 26.9%;  Pred. No. 3.4e-22;
ID   AAB27272 standard; protein; 310 AA.
DE   Human confluency regulated adhesion molecule 1 #1.
PN   WO200053749-A2.
PD   14-SEP-2000.
PA   (RMFD-) RMF DICTAGENE SA.

RESULT 836
  Best Local Similarity 33.8%;  Score 415;  DB 3;  Length 76;
  Query Match 26.9%;  Pred. No. 3.4e-22;
ID   ADK40850 standard; peptide; 76 AA.
DE   Human F11-adhesion molecule (FAM) conserved region #1.
PN   US6699688-B1.
PD   02-MAR-2004.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.

RESULT 837
  Best Local Similarity 100.0%;  Score 412;  DB 8;  Length 76;
  Query Match 26.7%;  Pred. No. 1.1e-22;
ID   ADU66690 standard; protein; 76 AA.
DE   Human FAM C2-type Ig domain #1.
PN   US2004235768-A1.
PD   25-NOV-2004.
PA   (KORN/) KORNECKI E.
PA   (SOBO/) SOBOCKA M B.

RESULT 838
  Best Local Similarity 33.1%;  Score 412;  DB 3;  Length 285;
  Query Match 26.7%;  Pred. No. 5.1e-22;
ID   AAB39254 standard; protein; 285 AA.
DE   Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
PN   WO200056754-A1.
PD   28-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 839
  Best Local Similarity 33.1%;  Score 412;  DB 8;  Length 76;
  Query Match 26.7%;  Pred. No. 1.1e-22;
ID   ADK40852 standard; peptide; 76 AA.
DE   Human F11-adhesion molecule (FAM) conserved region #2.
PN   US6699688-B1.
PD   02-MAR-2004.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.

RESULT 840
  Best Local Similarity 100.0%;  Score 409;  DB 8;  Length 76;
  Query Match 26.5%;  Pred. No. 1.8e-22;
ID   ADU66692 standard; protein; 76 AA.
DE   Human FAM C2-type Ig domain #2.
PN   US2004235768-A1.
PD   25-NOV-2004.
PA   (KORN/) KORNECKI E.
PA   (SOBO/) SOBOCKA M B.

RESULT 841
  Best Local Similarity 35.2%;  Score 409;  DB 2;  Length 312;
  Query Match 26.5%;  Pred. No. 2.2e-21;
ID   AAY08060 standard; protein; 312 AA.
DE   Human PRO245 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.

RESULT 842
  Best Local Similarity 35.2%;  Score 404;  DB 2;  Length 312;
  Query Match 26.2%;  Pred. No. 2.2e-21;
ID   AAY23324 standard; protein; 312 AA.
DE   A33 related antigen PRO245.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.

RESULT 843
  Best Local Similarity 35.2%;  Score 404;  DB 2;  Length 312;
  Query Match 26.2%;  Pred. No. 2.2e-21;
ID   AAY13354 standard; protein; 312 AA.
DE   Human PRO245 protein UNQ219 SEQ ID NO:36.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.

RESULT 844
  Best Local Similarity 35.2%;  Score 404;  DB 2;  Length 312;
  Query Match 26.2%;  Pred. No. 2.2e-21;
ID   AAB33421 standard; protein; 312 AA.
DE   Human PRO245 protein.
PN   WO200053758-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.

RESULT 845
  Best Local Similarity 35.2%;  Score 404;  DB 3;  Length 312;
  Query Match 26.2%;  Pred. No. 2.2e-21;
ID   AAY70668 standard; protein; 312 AA.
DE   Human PRO245 protein.
PN   WO200015797-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.

RESULT 846
  Best Local Similarity 35.2%;  Score 404;  DB 3;  Length 312;
  Query Match 26.2%;  Pred. No. 2.2e-21;
ID   AAB24401 standard; protein; 312 AA.
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DE Human PRO245 protein sequence SEQ ID NO:67.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 3; Pred. No. 2.2e-21;
RESULT 847
ID ADC78384 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 3; Length 312;
RESULT 848
ID AAB80222 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 3; Length 312;
RESULT 849
ID AAU00821 standard; protein; 312 AA.
DE Human immune response protein PRO245
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 4; Length 312;
RESULT 850
ID AAU12339 standard; protein; 312 AA.
DE Human PRO245 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 4; Length 312;
RESULT 851
ID AAB53081 standard; protein; 312 AA.
DE Human angiogenesis-associated protein PRO245 (UNQ219).
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 4; Length 312;
RESULT 852
ID ABU71600 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US20020146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 853
ID ABO17783 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20030032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 854
ID ABU71455 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US20020192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 855
ID ABU01037 standard; protein; 312 AA.
DE Human PRO polypeptide #168.

PN US20030043311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 856
ID ABU71901 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US20030035530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 857
ID ABO01784 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20021976711-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 858
ID ABU66737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20030303180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 859
ID ABU54357 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US20021324240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 860
ID ABO47372 standard; protein; 312 AA.
DE Human secreted/transmembrane polypeptide PRO245.
PN US20030449839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 861
ID ABU59818 standard; protein; 312 AA.
DE Novel secreted and transmembrane protein PRO245.
PN US20030175563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 862
ID ABO25008 standard; protein; 312 AA.
DE Human secreted/transmembrane protein (PRO) #168.
PN US20030036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 863
ID ABU64509 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20021603L4-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 35.2%;
Best Local Similarity 26.2%; Score 404; DB 6; Length 312;
RESULT 864
ID ABU67355 standard; protein; 312 AA.
DE Human secreted protein PRO245.
PN US20030203054-A1.

PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 865
ID   AB014875 standard; protein; 312 AA.
DE   Human secreted / transmembrane polypeptide PRO245.
PN   US2003030060-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 866
ID   ABU07738 standard; protein; 312 AA.
DE   Human A-33 related antigen PRO245.
PN   US2002182206-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 867
ID   ABU67013 standard; protein; 312 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 336.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 868
ID   ABU69632 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 869
ID   AB014814 standard; protein; 312 AA.
DE   Human secreted / transmembrane polypeptide PRO245.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 870
ID   ADA45855 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 871
ID   ADA76286 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 872
ID   ADB29269 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 873
ID   ADA18936 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 874
ID   ADA61559 standard; protein; 312 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 875
ID   ADB19344 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 876
ID   ADB27885 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 877
ID   ADA86364 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 878
ID   ADB15928 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 879
ID   ADA47714 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 880
ID   ADA18125 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 881
ID   AB032766 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein PRO245.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 882
ID   ADA67509 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 883
ID ADB30516 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 884
ID ADA85812 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 885
ID ADA97024 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 886
ID ADA79328 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 887
ID ADA7467 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 888
ID ADB16669 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 889
ID ABO34826 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 890
ID ADA16100 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 891
ID ADA91761 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%;

Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 892
ID ADB14824 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 893
ID ADB18785 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 894
ID ADA94000 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 895
ID ADB19896 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082691-A1.
PD 06-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 896
ID ADB13208 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 897
ID ABO43316 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 898
ID ADA74462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 899
ID ADA42245 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 900
ID ADB24695 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 6; Length 312;
Best Local Similarity 35.2%;

RESULT 901
ID ADA82219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 902
ID ADA75182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 903
ID ADA85260 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 904
ID ADA84708 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 905
ID ABO17504 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 906
ID ADB29964 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 907
ID ADA80492 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 908
ID ADA75734 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082703-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 909
ID ADA46959 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 910
ID ADB25255 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 911
ID ADA93431 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 912
ID ADB26781 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 913
ID ADB31068 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 914
ID ADA60996 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 915
ID ADB24143 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 916
ID ADA96472 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 917
ID ADA81044 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 918
ID ADA95920 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%;
Best Local Similarity 35.2%;
Score 404; DB 6; Length 312;
Pred. No. 2.2e-21;

RESULT 919
ID ADB26229 standard; protein; 312 AA.

DE   Human PRO polypeptide #168.
PN   US20030082760-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 920
ID   ADB21714 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030082765-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 6; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 921
ID   ADA77493 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030068797-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 922
ID   ADB18233 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030077710-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 923
ID   ADA86916 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030082709-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 924
ID   ADA16524 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030039969-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 925
ID   ADA12953 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030049622-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 926
ID   ADA41821 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030082540-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 927
ID   ADA88019 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030082700-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 928
ID   ADA64607 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.

PN   US20030054516-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 929
ID   ADA42671 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030054351-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 930
ID   ADA17168 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030017498-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 931
ID   ADB24437 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030082699-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 932
ID   ADB28989 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030082706-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 933
ID   ADA76941 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030059909-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 934
ID   ADA85571 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030072213-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 935
ID   ADA97576 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030082686-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 936
ID   ADB27333 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030022239-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;

RESULT 937
ID   ADB22266 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030087344-A1.
PD   08-MAY-2003.

```
Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 938              35.2%;   Pred. No. 2.2e-21;
ID  AB017565 standard; protein; 312 AA.
DE  Human PRO polypeptide #11.
PN  US20030064923-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 939              35.2%;   Pred. No. 2.2e-21;
ID  ADA66957 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030068793-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 940              35.2%;   Pred. No. 2.2e-21;
ID  ADB22818 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030077711-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 941              35.2%;   Pred. No. 2.2e-21;
ID  ADB23591 standard; protein; 312 AA.
DE  Human PRO polypeptide SEQ ID NO 336.
PN  US20030077712-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 942              35.2%;   Pred. No. 2.2e-21;
ID  ADA92313 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082712-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 943              35.2%;   Pred. No. 2.2e-21;
ID  ADB15376 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030087352-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 944              35.2%;   Pred. No. 2.2e-21;
ID  ADB38628 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030087347-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 945              35.2%;   Pred. No. 2.2e-21;
ID  ADB30076 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082766-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 946              35.2%;   Pred. No. 2.2e-21;
ID  ADB66548 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082689-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   35.2%;   Pred. No. 2.2e-21;
RESULT 947
ID  ADB89628 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030082698-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 948              35.2%;   Pred. No. 2.2e-21;
ID  ADB90360 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030082762-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 949              35.2%;   Pred. No. 2.2e-21;
ID  ADB77590 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein, #13.
PN  US20030077654-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 950              35.2%;   Pred. No. 2.2e-21;
ID  ADB39461 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082764-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 951              35.2%;   Pred. No. 2.2e-21;
ID  ADB74726 standard; protein; 312 AA.
DE  Human secreted/transmembrane protein, #13.
PN  US20030082542-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 952              35.2%;   Pred. No. 2.2e-21;
ID  ADB47084 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082687-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 953              35.2%;   Pred. No. 2.2e-21;
ID  ADB86691 standard; protein; 312 AA.
DE  Human PRO polypeptide #168.
PN  US20030082696-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 954              35.2%;   Pred. No. 2.2e-21;
ID  ADB77296 standard; protein; 312 AA.
DE  Novel human secreted and transmembrane protein PRO245.
PN  US20030082697-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
RESULT 955              35.2%;   Pred. No. 2.2e-21;
ID  ADB34453 standard; protein; 312 AA.
DE  Human PRO polypeptide SEQ ID NO 336.
PN  US20030077717-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.

Query Match
Best Local Similarity   26.2%;   Score 404;   DB 7;   Length 312;
```

RESULT 956
ID ADB35557 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 957
ID ADB33901 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 958
ID ADB35005 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 959
ID ADB36109 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 960
ID ADB46504 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 961
ID ADC28372 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 962
ID ADC39572 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 963
ID ADC40086 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 964
ID ADC18914 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 965
ID ADC59903 standard; protein; 312 AA.

ID ADC34210 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 966
ID ADC29265 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 967
ID ADC28796 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 968
ID ADC40681 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 969
ID ADC19938 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 970
ID ADC33786 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 971
ID ADC12856 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 972
ID ADC50377 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 973
ID ADC71924 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 974
ID ADC59903 standard; protein; 312 AA.

DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030092105-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
PD   Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
PD   Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 975
ID   ADCS2910 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087365-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 976
ID   ADC57264 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087366-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 977
ID   ADC60455 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087367-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 978
ID   ADC50930 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030087361-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 979
ID   ADC65457 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030087362-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 980
ID   ADC54555 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087363-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 981
ID   ADC53516 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087364-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 982
ID   ADCS9039 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087359-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 983
ID   ADCS5917 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030092103-A1.

PN   US20030087360-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 984
ID   ADC58487 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein Seq ID336.
PN   US20030087346-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 985
ID   ADC12308 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030082541-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 986
ID   ADD03161 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030092104-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 987
ID   ADC90153 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030087348-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 988
ID   ADC69572 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030194770-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 989
ID   ADC48461 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030194773-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 990
ID   ADD09990 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20030194776-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 991
ID   ADD04565 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030087354-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 35.2%;   Score 404; DB 7; Length 312;
     Query Match 26.2%;   Pred. No. 2.2e-21;

RESULT 992
ID   ADC80521 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030092103-A1.

PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 993
ID   ADD11028 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319477 4-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 994
ID   ADC47909 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein #13.
PN   US200319477 1-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 995
ID   ADD04863 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein, #13.
PN   US200310446 9-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 996
ID   ADC79969 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US200308735 8-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 997
ID   ADD09438 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319477 5-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 998
ID   ADD03869 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US200310438 1-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 999
ID   ADD03445 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein #13.
PN   US200310898 3-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1000
ID   ADD41151 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US200320343 8-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1001
ID   ADD52290 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319476 9-A1.
PD   16-OCT-2003.

PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1002
ID   ADD53030 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319479 2-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1003
ID   ADD53582 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US200320343 7-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1004
ID   ADD51738 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319477 9-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1005
ID   ADD02537 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200320343 1-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1006
ID   ADD01971 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US200320343 0-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1007
ID   ADD54153 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US200320343 2-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1008
ID   ADD92470 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319903 0-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1009
ID   ADD91366 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319905 5-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1010
ID   ADE09980 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US200319905 7-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1011
ID ADB32277 standard; protein; 312 AA.
DE Human secreted and transmembrane protein PRO245.
PN US200319476S-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
PD 23-OCT-2003.
PA
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1012
ID ADE22209 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319905G-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
PD 30-OCT-2003.
PA
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1013
ID ADD79433 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200320342B-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1014
ID ADE41969 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319477Z-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1015
ID ADE17786 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20031990Z3-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1016
ID ADD91918 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20031990S3-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1017
ID ADE33381 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319476Z-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1018
ID ADE33933 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US200319479I-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1019
ID ADD79985 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20032074I7-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;

Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1020
ID ADD93022 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319476B-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1021
ID ADE19442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319902S-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1022
ID ADE34697 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20030775B3-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1023
ID ADE18890 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20031990Z6-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1024
ID ADE43086 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20031990S3-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1025
ID ADD95875 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200319905S-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1026
ID ADE22761 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20031990G4-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1027
ID ADD78879 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032034Z9-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.2e-21;
RESULT 1028
ID ADE32829 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US200319476G-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 35.2%; Score 404; DB 7; Length 312;
Best Local Similarity 26.2%;

RESULT 1029
ID   ADE42521 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1030
ID   ADD80537 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1031
ID   ADD89565 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1032
ID   ADE40849 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1033
ID   ADE04648 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1034
ID   ADE92777 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1035
ID   ADG21486 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1036
ID   ADG23127 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1037
ID   ADF97462 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;

RESULT 1038

ID   ADG80526 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1039
ID   ADG79974 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1040
ID   ADH62536 standard; protein; 312 AA.
DE   Human PRO245 protein encoded by DNA35638 cDNA.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1041
ID   ADH59180 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1042
ID   ADH55266 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1043
ID   ADH55818 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1044
ID   ADI37959 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein #13.
PN   US2003054552-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1045
ID   ADI64986 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%;   Score 404;   DB 7;   Length 312;
Best Local Similarity 35.2%;   Pred. No. 2.2e-21;

RESULT 1046
ID   ADH81899 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207388-A1.

PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1047
ID   ADH81347 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1048
ID   ADJ26227 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20030543349-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1049
ID   ADM82516 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1050
ID   ADN15915 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1051
ID   ADN16544 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1052
ID   ADN15363 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1053
ID   ADN14811 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1054
ID   ADI64037 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1055
ID   ADI63485 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207337-A1.
PD   06-NOV-2003.

PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1056
ID   ADC81073 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1057
ID   ADE79142 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1058
ID   ADD76521 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 7; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1059
ID   ADD87885 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1060
ID   ADD86289 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1061
ID   ADE79566 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1062
ID   ADE75737 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003121571-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1063
ID   ADE73242 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;
RESULT 1064
ID   ADE23313 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.

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Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1065
ID   ADE23865 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1066
ID   ADE24508 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1067
ID   ADE87333 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1068
ID   ADB89199 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1069
ID   ADF73777 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1070
ID   ADE18338 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1071
ID   ADE88647 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1072
ID   ADE99331 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1073
ID   ADE94667 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;


Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1074
ID   ADE91078 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1075
ID   ADE95219 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1076
ID   ADE93329 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1077
ID   ADF34910 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1078
ID   ADB98450 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1079
ID   ADE92225 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1080
ID   ADE90526 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1081
ID   ADE91673 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003199058-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
RESULT 1082
ID   ADE98877 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match    26.2%;  Score 404;  DB 8;  Length 312;
Best Local Similarity    35.2%;  Pred. No. 2.2e-21;
```

RESULT 1083
ID ADG40347 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20032252253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1084
ID ADF73741 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20032180312-A1.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1085
ID ADG22252 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1086
ID ADG22038 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20032207360-A1.
PD 06-NOV-2003.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1087
ID ADG20108 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1088
ID ADF98014 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1089
ID ADG24231 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20032207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1090
ID ADF98585 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1091
ID ADG03416 standard; protein; 312 AA.
DE Human PRO polypeptide #168.

PN US20032207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1092
ID ADF99137 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1093
ID ADG16722 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1094
ID ADG05181 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1095
ID ADG19448 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1096
ID ADF73317 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031666051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1097
ID ADG13285 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1098
ID ADG08342 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20032207424-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1099
ID ADG15512 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032219885-A1.
PD
  Query Match 26.2%; Score 404; DB 8; Length 312;
  Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1100
ID ADF96910 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20032207371-A1.

PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1101
ID   ADG06095 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20032071374-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1102
ID   ADG23679 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071389-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1103
ID   ADG03968 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20032071423-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1104
ID   ADG24869 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071427-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1105
ID   ADG07166 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071350-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1106
ID   ADG07718 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071356-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1107
ID   ADG55213 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20031947778-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1108
ID   ADG60877 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071390-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1109
ID   ADG61981 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071428-A1.
PD   06-NOV-2003.

PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1110
ID   ADG92160 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20032071145-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1111
ID   ADG82182 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20032071358-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1112
ID   ADG57421 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071362-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1113
ID   ADG56869 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071364-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1114
ID   ADG55765 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071365-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1115
ID   ADG58525 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071368-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1116
ID   ADG70891 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071420-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1117
ID   ADG92587 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US20032071146-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
RESULT 1118
ID   ADG57973 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20032071363-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

RESULT 1119
ID   ADG53557 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1120
ID   ADG71443 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1121
ID   ADG81630 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1122
ID   ADH30592 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1123
ID   ADH11959 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1124
ID   ADG52381 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1125
ID   ADG54109 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1126
ID   ADG81078 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1127
ID   ADG56317 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1128
ID   ADH12583 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1129
ID   ADG61429 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1130
ID   ADG28516 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1131
ID   ADG59701 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1132
ID   ADH20376 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1133
ID   ADH07231 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1134
ID   ADH59776 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2004006211-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1135
ID   ADH06804 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

RESULT 1136
Query Match
Best Local Similarity 35.2%;   Score 404;   DB 8;   Length 312;

PN US20040005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1137
ID ADI81125 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US20030207361-A1.
PD 06-NOV-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1138
ID ADI18546 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031152999-A1.
PD 14-AUG-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1139
ID ADI65266 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031148419-A1.
PD 07-AUG-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1140
ID ADI37529 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20030963340-A1.
PD 22-MAY-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1141
ID ADG9868 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20040009548-A1.
PD 15-JAN-2004.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1142
ID ADH7333 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031190610-A1.
PD 09-OCT-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1143
ID ADI15339 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20030207382-A1.
PD 06-NOV-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1144
ID ADG9216 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20040009547-A1.
PD 15-JAN-2004.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1145
ID ADI14671 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20030207383-A1.
PD 06-NOV-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1146
ID ADH60436 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20040023331-A1.
PD 05-FEB-2004.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1147
ID ADI18266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20032073349-A1.
PD 06-NOV-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1148
ID ADJ99493 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031187238-A1.
PD 02-OCT-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1149
ID ADI08686 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031186358-A1.
PD 02-OCT-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1150
ID ADM25031 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20030962233-A1.
PD 22-MAY-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1151
ID ADJ63547 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20040039164-A1.
PD 26-FEB-2004.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1152
ID ADM29777 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031190611-A1.
PD 09-OCT-2003.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity   35.2%; Pred. No. 2.2e-21;
PA (GETH) GENENTECH INC.

RESULT 1153

ID   ADJ77442 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20040338336-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1154
ID   ADJ65564 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20040338335-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1155
ID   ADM27700 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20040048333-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1156
ID   ADM42424 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20040058424-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1157
ID   ADO06099 standard; protein; 312 AA.
DE   Human PRO polypeptide #11.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1158
ID   ADN35292 standard; protein; 312 AA.
DE   Human PRO245 protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1159
ID   ADM28286 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US20040077064-A1.
PD   22-APR-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1160
ID   ADR10951 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1161
ID   ADR17860 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1162
ID   ADI95768 standard; protein; 312 AA.
DE   Human PRO polypeptide #168.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1163
ID   ADI96320 standard; protein; 312 AA.
DE   Novel human secreted and transmembrane protein PRO245.
PN   US20030207354-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1164
ID   ADI65693 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein, #13.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1165
ID   ADI94237 standard; protein; 312 AA.
DE   Human PRO245 protein.
PN   AU2003259607-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   26.2%; Score 404; DB 8; Length 312;
Best Local Similarity 35.2%; Pred. No. 2.2e-21;

RESULT 1166
ID   ADS74499 standard; protein; 312 AA.
DE   Human secreted/transmembrane protein #13.
PN   US2004185531-A1.
PD   23-SEP-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.

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PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
    Query Match
    Best Local Similarity   26.2%;   Score 404;  DB 9;  Length 312;

RESULT 1167
ID ADS322272 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US20040203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   35.2%;   Pred. No. 2.2e-21;

RESULT 1168
ID ADT03256 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200421269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   26.2%;   Score 404;  DB 8;  Length 312;

RESULT 1169
ID ADT03536 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20031529222-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   35.2%;   Pred. No. 2.2e-21;

RESULT 1170
ID AD203307 standard; protein; 312 AA.
DE Human secreted/transmembrane PRO245 protein.
PN US20050074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   26.2%;   Score 404;  DB 8;  Length 312;

RESULT 1171
ID AEA37774 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US20051127225-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   35.2%;   Pred. No. 2.2e-21;

RESULT 1172
ID AEB14053 standard; protein; 312 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 336.
PN US20051533396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
    Query Match
    Best Local Similarity   26.2%;   Score 404;  DB 9;  Length 312;

RESULT 1173
ID ADP56682 standard; protein; 323 AA.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (BLIL ) LILLY & CO ELI.
    Query Match
    Best Local Similarity   35.2%;   Pred. No. 2.3e-21;

RESULT 1174
ID AAB50904 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
    Query Match
    Best Local Similarity   26.0%;   Score 402;  DB 4;  Length 312;

RESULT 1175
ID AAM41947 standard; protein; 222 AA.
DE Human polypeptide SEQ ID NO 6878.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
    Query Match
    Best Local Similarity   25.9%;   Score 399.5;  DB 4;  Length 222;

RESULT 1176
ID AAB70500 standard; protein; 215 AA.
DE Angiogenesis protein AAA1 protein sequence (Fig 8).
PN WO200111086-A2.
PD 15-FEB-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
    Query Match
    Best Local Similarity   25.6%;   Score 395.5;  DB 4;  Length 215;

RESULT 1177
ID AAB27277 standard; protein; 213 AA.
DE Human confluency regulated adhesion molecule #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
    Query Match
    Best Local Similarity   25.6%;   Score 392.5;  DB 3;  Length 213;

RESULT 1178
ID AAB27273 standard; protein; 298 AA.
DE Human confluency regulated adhesion molecule 2 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
    Query Match
    Best Local Similarity   39.7%;   Score 391;  DB 3;  Length 298;

RESULT 1179
ID AAB27275 standard; protein; 298 AA.
DE Murine confluency regulated adhesion molecule 2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
    Query Match
    Best Local Similarity   39.4%;   Score 391;  DB 3;  Length 298;

RESULT 1180
ID AAB06037 standard; protein; 321 AA.
DE Human NS protein sequence SEQ ID NO:129.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
    Query Match
    Best Local Similarity   25.3%;   Score 389;  DB 5;  Length 321;

RESULT 1181
ID ABG22341 standard; protein; 388 AA.
DE Novel human diagnostic protein #22332.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
    Query Match
    Best Local Similarity   25.1%;   Score 387.5;  DB 4;  Length 388;
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Best Local Similarity   34.2%;   Pred. No. 4.6e-20;
PA   (CATC-) CATCHMABS BV.
PD   11-JUN-2003.
PN   EP1318195-A1.
DE   Murine junction adhesion molecule protein used to create novel VAPs.
ID   ADF17957 standard; protein; 102 AA.
RESULT 1182

Query Match   23.8%;   Score 367; DB 7;   Length 259;
Best Local Similarity   66.0%;   Pred. No. 3e-19;
PA   (HUMA-) RES ASSOC BIOTECHNOLOGY.
PD   28-JUL-2004.
PN   EP1400981-A2.
DE   Novel human protein sequence #648.
ID   ADQ65675 standard; protein; 259 AA.
RESULT 1183

Query Match   22.8%;   Score 351.5; DB 8;   Length 235;
Best Local Similarity   38.1%;   Pred. No. 1.2e-17;
PA   (GEST) GENSET SA.
PD   05-JUN-2003.
PN   WO2003046180-A2.
DE   Human novel splice variant of VEJAM (NoJAM).
ID   AAO30179 standard; protein; 235 AA.
RESULT 1184

Query Match   22.1%;   Score 341.5; DB 6;   Length 265;
Best Local Similarity   32.9%;   Pred. No. 5.9e-17;
PA   (ELIL) LILLY & CO ELI.
PD   24-JUN-2004.
PN   WO2004053058-A2.
DE   Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) protein.
ID   ADP56685 standard; protein; 265 AA.
RESULT 1185

Query Match   21.1%;   Score 326.5; DB 8;   Length 265;
Best Local Similarity   32.9%;   Pred. No. 8.5e-16;
PA   (INCY-) INCYTE CORP.
PD   04-NOV-2004.
PN   WO2004094623-A2.
DE   Cell adhesion and extracellular matrix protein clone 7518734CD1.
ID   ADU06841 standard; protein; 265 AA.
RESULT 1186

Query Match   21.1%;   Score 326.5; DB 8;   Length 238;
Best Local Similarity   32.9%;   Pred. No. 8.5e-16;
PA   (RMFD-) RMF DICTAGENE SA.
PA   (UYPE-) UNIV PENNSYLVANIA.
PD   23-OCT-2003.
PN   WO2003087128-A2.
DE   Human adhesion molecule JAM-2.
ID   ADF12431 standard; protein; 238 AA.
RESULT 1187

Query Match   21.0%;   Score 325; DB 8;   Length 238;
Best Local Similarity   33.1%;   Pred. No. 9.7e-16;
PA   (RMFD-) RMF DICTAGENE SA.
PA   (UYPE-) UNIV PENNSYLVANIA.
PD   18-DEC-2003.
PN   WO2003104400-A2.
DE   Human JAM-2 protein SEQ ID NO:18.
ID   ADG39949 standard; protein; 238 AA.
RESULT 1188

Query Match   21.0%;   Score 325; DB 4;   Length 361;
Best Local Similarity   33.1%;   Pred. No. 9.7e-16;
PA   (HYSE-) HYSEQ INC.
PD   11-OCT-2001.
PN   WO200175067-A2.
DE   Novel human diagnostic protein #22392.
ID   ABG22401 standard; protein; 361 AA.
RESULT 1189

Query Match   20.4%;   Score 315; DB 4;   Length 105;
Best Local Similarity   33.0%;   Pred. No. 8.5e-15;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   02-AUG-2001.
PN   WO200155315-A2.
DE   Human immunoglobulin polypeptide SEQ ID No 152.
ID   AAU18007 standard; protein; 105 AA.
RESULT 1190

Query Match   20.1%;   Score 310.5; DB 4;   Length 105;
Best Local Similarity   66.7%;   Pred. No. 4.3e-15;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   02-AUG-2001.
PN   WO200155320-A2.
DE   Human reproductive system related antigen SEQ ID NO: 4990.
ID   AAM96332 standard; protein; 105 AA.
RESULT 1191

Query Match   20.1%;   Score 310.5; DB 4;   Length 105;
Best Local Similarity   66.7%;   Pred. No. 4.3e-15;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   02-AUG-2001.
PN   WO200154474-A2.
DE   Human cDNA SEQ ID NO: 744.
ID   ABB10436 standard; protein; 105 AA.
RESULT 1192

Query Match   20.1%;   Score 310.5; DB 5;   Length 105;
Best Local Similarity   66.7%;   Pred. No. 4.3e-15;
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (BARA/) BARASH S C.
PD   11-JUL-2002.
PN   US2002090672-A1.
DE   Human polypeptide SEQ ID NO 744.
ID   ABP67023 standard; protein; 105 AA.
RESULT 1193

Query Match   20.1%;   Score 310.5; DB 7;   Length 105;
Best Local Similarity   66.7%;   Pred. No. 4.3e-15;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   24-APR-2003.
PN   US2003077606-A1.
DE   Human novel protein SEQ ID NO 152.
ID   ADB31631 standard; protein; 105 AA.
RESULT 1194

Query Match   19.8%;   Score 305; DB 8;   Length 206;
Best Local Similarity   34.0%;   Pred. No. 2.4e-14;
PA   (CURA-) CURAGEN CORP.
PD   01-JUL-2004.
PN   WO2004055158-A2.
DE   Human NOV2a mature extracellular domain protein SEQ ID NO:68.
ID   ADP69098 standard; protein; 206 AA.
RESULT 1195

Query Match   19.8%;   Score 305; DB 8;   Length 206;
Best Local Similarity   34.0%;   Pred. No. 2.4e-14;
PA   (CURA-) CURAGEN CORP.
PD   01-JUL-2004.
PN   WO2004055158-A2.
DE   Human NOV2d protein SEQ ID NO:26.
ID   ADP69031 standard; protein; 206 AA.
RESULT 1196

Query Match   19.8%;   Score 305; DB 8;   Length 206;
Best Local Similarity   34.0%;   Pred. No. 2.4e-14;
PA   (CURA-) CURAGEN CORP.
PD   01-JUL-2004.
PN   WO2004055158-A2.
DE   Human NOV2c protein SEQ ID NO:24.
ID   ADP69029 standard; protein; 206 AA.
RESULT 1197

Query Match   19.8%;   Score 305; DB 8;   Length 318;
Best Local Similarity   34.0%;   Pred. No. 1.3e-12;
PA   (LUDW-) LUDWIG INST CANCER RES.
PD   06-MAR-1997.
PN   WO9708189-A1.
DE   Mouse A33 antigen.
ID   AAW14158 standard; protein; 318 AA.
RESULT 1198

Query Match   18.4%;   Score 284.5; DB 2;   Length 229;
Best Local Similarity   29.5%;   Pred. No. 1.3e-12;
PA   (ELIL) LILLY & CO ELI.
PD   24-JUN-2004.
PN   WO2004053058-A2.
DE   Human junction adhesion molecule 3 splice variant 1 (huJAM3sv1) protein.
ID   ADP56684 standard; protein; 229 AA.
RESULT 1199

PA (ELIL) LILLY & CO ELI.
Query Match   18.3%;   Score 282;   DB 8;   Length 229;
Best Local Similarity 33.3%;   Pred. No. 1.3e-12;
RESULT 1200
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
PN US5699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match   18.1%;   Score 279;   DB 8;   Length 316;
Best Local Similarity 26.5%;   Pred. No. 3.1e-12;
RESULT 1201
ID ADU66694 standard; protein; 316 AA.
DE Human A33 protein.
PN US20042355768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match   18.1%;   Score 279;   DB 8;   Length 316;
Best Local Similarity 26.5%;   Pred. No. 3.1e-12;
RESULT 1202
ID ABG22338 standard; protein; 140 AA.
DE Novel human diagnostic protein #22329.
PN WO20017567-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match   17.9%;   Score 276;   DB 4;   Length 140;
Best Local Similarity 40.1%;   Pred. No. 2e-12;
RESULT 1203
ID AAW1416 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match   17.6%;   Score 272.5; DB 2;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1204
ID AAY23323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272.5; DB 4;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1205
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO20007808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   17.6%;   Score 272.5; DB 2;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1206
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US20021603822-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match   17.6%;   Score 272.5; DB 6;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1207
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US20031571568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match   17.6%;   Score 272.5; DB 7;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1208
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match   17.6%;   Score 272.5; DB 7;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1209
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272.5; DB 8;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1210
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO:563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272.5; DB 8;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1211
ID AEB85134 standard; protein; 319 AA.
DE Human novel secreted protein huA33.
PN WO2005058028-A2.
PD 30-JUN-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match   17.6%;   Score 272.5; DB 9;   Length 319;
Best Local Similarity 25.8%;   Pred. No. 9.5e-12;
RESULT 1212
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN WO2002018424-A2.
PD 07-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272.5; DB 5;   Length 336;
Best Local Similarity 25.8%;   Pred. No. 1e-11;
RESULT 1213
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272;   DB 2;   Length 273;
Best Local Similarity 26.8%;   Pred. No. 8.6e-12;
RESULT 1214
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match   17.6%;   Score 272;   DB 2;   Length 273;
Best Local Similarity 26.8%;   Pred. No. 8.6e-12;
RESULT 1215
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US20031571568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match   17.6%;   Score 272;   DB 7;   Length 273;
Best Local Similarity 26.8%;   Pred. No. 8.6e-12;

RESULT 1216
ID   AAY08073 standard; protein; 268 AA.
DE   Human A33 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH) GENENTECH INC.
  Query Match   17.4%; Score 269; DB 2; Length 268;
  Best Local Similarity   26.6%; Pred. No. 1,4e-11;

RESULT 1217
ID   ADH62551 standard; protein; 268 AA.
DE   Human A33 antigenic protein fragment #1.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
  Query Match   17.4%; Score 269; DB 7; Length 268;
  Best Local Similarity   26.6%; Pred. No. 1,4e-11;

RESULT 1218
ID   AAY23327 standard; protein; 270 AA.
DE   An A33 related antigen sequence.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH) GENENTECH INC.
  Query Match   17.4%; Score 269; DB 2; Length 270;
  Best Local Similarity   26.6%; Pred. No. 1,4e-11;

RESULT 1219
ID   AAO11807 standard; protein; 134 AA.
DE   Human polypeptide SEQ ID NO 25699.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match   15.6%; Score 240.5; DB 4; Length 134;
  Best Local Similarity   86.7%; Pred. No. 7.6e-10;

RESULT 1220
ID   ABG04645 standard; protein; 291 AA.
DE   Novel human diagnostic protein #4636.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match   15.1%; Score 233.5; DB 4; Length 291;
  Best Local Similarity   32.9%; Pred. No. 6.1e-09;

RESULT 1221
ID   ABM84859 standard; protein; 344 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5108.
PN   WO2004023973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match   15.1%; Score 233; DB 8; Length 344;
  Best Local Similarity   28.1%; Pred. No. 7.4e-09;

RESULT 1222
ID   ABG12109 standard; protein; 404 AA.
DE   Novel human diagnostic protein #12100.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match   15.1%; Score 233.5; DB 4; Length 404;
  Best Local Similarity   32.9%; Pred. No. 8.9e-09;

RESULT 1223
ID   AAY87251 standard; protein; 327 AA.
DE   Human signal peptide containing protein HSPP-28 SEQ ID NO:28.
PN   WO200000610-A2.
PD   06-JAN-2000.
PA   (INCY-) INCYTE PHARM INC.
  Query Match   15.0%; Score 232; DB 3; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1224
ID   AAY94857 standard; protein; 327 AA.
DE   Human protein clone HP10568.

PN   WO200005367-A2.
PD   03-FEB-2000.
PA   (SAGA) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
  Query Match   15.0%; Score 232; DB 3; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1225
ID   AAB08903 standard; protein; 327 AA.
DE   Human secreted protein sequence encoded by gene 13 SEQ ID NO:60.
PN   WO200017222-A1.
PD   30-MAR-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match   15.0%; Score 232; DB 3; Length 327;
  Best Local Similarity   30.1%; Pred. No. 9e-09;

RESULT 1226
ID   AAY97585 standard; protein; 327 AA.
DE   Human secreted protein PRO7154.
PN   WO200075317-A2.
PD   14-DEC-2000.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 4; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1227
ID   ABB90354 standard; protein; 327 AA.
DE   Human polypeptide SEQ ID NO 2730.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match   15.0%; Score 232; DB 5; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1228
ID   AAU83709 standard; protein; 327 AA.
DE   Human PRO protein, Seq ID No 236.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 5; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1229
ID   ADY31976 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   WO200193983-A1.
PD   13-DEC-2001.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 5; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1230
ID   ABU80856 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US20030036635-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 6; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1231
ID   ABO33822 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US20030045687-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 6; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1232
ID   ABU82165 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US20030088063-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
  Query Match   15.0%; Score 232; DB 6; Length 327;
  Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1233
ID   ABJ72345 standard; protein; 327 AA.
DE   Human PRO7154 protein.

PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 6; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1234
ID   ABJ72473 standard; protein; 327 AA.
DE   Human PRO7154 protein.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 6; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1235
ID   ABO4368 standard; protein; 327 AA.
DE   Human secreted/transmembrane protein; 327 AA.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 6; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1236
ID   ABJ72175 standard; protein; 327 AA.
DE   Human membrane bound receptor/protein PRO7154 amino acid sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1237
ID   ADB83726 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1238
ID   ADB80832 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1239
ID   ADB73373 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1240
ID   ADB78455 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1241
ID   ADB85103 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1242
ID   ADB78209 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003092886-A1.
PD   08-MAY-2003.

PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1243
ID   ADB87275 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1244
ID   ADB84857 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1245
ID   ADB83972 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003069337-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1246
ID   ADB73127 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1247
ID   ADC36965 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1248
ID   ADC21955 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1249
ID   ADC49986 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1250
ID   ADC49185 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   15.0%; Score 232; DB 7; Length 327;
     Best Local Similarity   29.4%; Pred. No. 9e-09;

RESULT 1251
ID   ADC49702 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088071-A1.
PD   08-MAY-2003.

PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1252
ID   ADC47563 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1253
ID   ADC47308 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1254
ID   ADC78183 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1255
ID   ADC06418 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1256
ID   ADC77937 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1257
ID   ADD50900 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1258
ID   ADD51146 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1259
ID   ADD50627 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 7; Pred. No. 9e-09; Length 327;
RESULT 1260
ID   ADD50381 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1261
ID   ADD51392 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1262
ID   ADC48939 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1263
ID   ADE21110 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1264
ID   ADE05954 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1265
ID   ADE05183 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1266
ID   ADD75929 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1267
ID   ADD85161 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1268
ID   ADD86987 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   15.0%;
     29.4%; Score 232; DB 8; Pred. No. 9e-09; Length 327;
RESULT 1269
ID   ADE20864 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match

Best Local Similarity   29.4%;   Pred. No. 9e-09;
RESULT 1270
ID   ADE39161 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity
RESULT 1271
ID   ADE05708 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1272
ID   ADD73693 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1273
ID   ADD78533 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1274
ID   ADE21356 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1275
ID   ADD77471 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1276
ID   ADE20618 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1277
ID   ADD75683 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1278
ID   ADD74199 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;

RESULT 1279
ID   ADD74445 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1280
ID   ADD76175 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1281
ID   ADD85667 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1282
ID   ADE05216 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1283
ID   ADD75429 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1284
ID   ADD76973 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1285
ID   ADD86741 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1286
ID   ADD78209 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1287
ID   ADD77717 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   29.4%;   Score 232;   DB 8;   Length 327;
Best Local Similarity   15.0%;   Pred. No. 9e-09;
RESULT 1288

ID   ADD77963 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
PN   US2003100725-A1.
DE   Novel human secreted and transmembrane protein PRO7154.
ID   ADD85421 standard; protein; 327 AA.
RESULT 1289
Best Local Similarity 29.4%;
Query Match 15.0%;   Score 232; DB 8; Length 327;
                Pred. No. 9e-09;
PA   (GETH) GENENTECH INC.
PD   29-MAY-2003.

ID   ADD73953 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1290
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADD74691 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1291
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADD77219 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1292
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADD85913 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1293
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADE05462 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1294
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADD74937 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096559-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1295
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADG05749 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096559-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1296
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232;   Length 327;

ID   ADG27303 standard; protein; 327 AA.
RESULT 1297

DE   Human PRO polypeptide #118.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1298
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADG11366 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1299
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADG12145 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1300
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADF94702 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1301
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADG06798 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1302
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADH39142 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1303
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADG34232 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
RESULT 1304
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADI33702 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1305
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADH69796 standard; protein; 327 AA.
DE   Human PRO polypeptide #118.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH) GENENTECH INC.
RESULT 1306
Best Local Similarity 29.4%; Pred. No. 9e-09;
Query Match 15.0%;   Score 232; DB 8; Length 327;

ID   ADI29957 standard; protein; 327 AA.
DE   Novel human secreted and transmembrane protein PRO7154.

PN US20030096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1307
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
ID ADM27354 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US20040044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
RESULT 1308
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
ID ADK66712 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US20040044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
RESULT 1309
Query Match 15.0%; Score 232; DB 8; Length 327;
Best Local Similarity 29.4%; Pred. No. 9e-09;
ID AAG75613 standard; protein; 365 AA.
DE Human colon cancer antigen protein SEQ ID NO:6377.
PN WO20012220-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 1310
Query Match 15.0%; Score 232; DB 3; Length 365;
Best Local Similarity 29.4%; Pred. No. 1e-08;
ID AAB53307 standard; protein; 365 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:847.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 1311
Query Match 14.8%; Score 229; DB 4; Length 365;
Best Local Similarity 28.8%; Pred. No. 1e-08;
ID ADF93097 standard; protein; 326 AA.
DE Human cortical thymocyte receptor CTXL, overexpressed in cancer.
PN WO2003100000-A2.
PD 04-DEC-2003.
PA (TULA-) TULARIK INC.
RESULT 1312
Query Match 14.7%; Score 227; DB 8; Length 326;
Best Local Similarity 28.8%; Pred. No. 1.5e-08;
ID ADK40847 standard; peptide; 42 AA.
DE Human platelet F11-adhesion molecule (FAM), peptide #1.
PN US5699688-B1.
PD 02-MAR-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
RESULT 1313
Query Match 14.7%; Score 227; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
ID ADU66687 standard; peptide; 42 AA.
DE Human FAM GluC-(4) peptide.
PN US20042235768-A1.
PD 25-NOV-2004.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
RESULT 1314
Query Match 14.7%; Score 227; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
ID AAW31100 standard; peptide; 50 AA.
DE Platelet membrane glycoprotein F11 fragment.
PN US5665701-A.
PD 09-SEP-1997.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
RESULT 1315
Query Match 14.7%; Score 227; DB 2; Length 50;
Best Local Similarity 89.8%; Pred. No. 2.3e-09;
ID AAB61480 standard; protein; 325 AA.
DE Human CTH protein.

PN WO20010672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
RESULT 1316
Query Match 14.6%; Score 225; DB 4; Length 325;
Best Local Similarity 28.5%; Pred. No. 2.9e-08;
ID ADG39844 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #5.
PN US20020203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
RESULT 1317
Query Match 13.9%; Score 214.5; DB 8; Length 1708;
Best Local Similarity 29.2%; Pred. No. 1.2e-06;
ID ADS10483 standard; protein; 2537 AA.
DE Human therapeutic protein - SEQ ID 720.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
RESULT 1318
Query Match 13.9%; Score 214.5; DB 8; Length 2537;
Best Local Similarity 29.2%; Pred. No. 1.9e-06;
ID ADS98860 standard; protein; 2537 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1124.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
RESULT 1319
Query Match 13.9%; Score 214.5; DB 8; Length 2537;
Best Local Similarity 29.2%; Pred. No. 1.9e-06;
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
RESULT 1320
Query Match 13.9%; Score 214.5; DB 6; Length 2572;
Best Local Similarity 29.2%; Pred. No. 1.9e-06;
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
RESULT 1321
Query Match 13.9%; Score 214; DB 8; Length 2673;
Best Local Similarity 29.2%; Pred. No. 2e-06;
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
RESULT 1322
Query Match 13.9%; Score 214; DB 8; Length 2673;
Best Local Similarity 29.2%; Pred. No. 2e-06;
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.

PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
    Query Match
    Best Local Similarity 13.9%; Score 214.5; DB 8; Length 2673; Pred. No. 2e-06;

RESULT 1323
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
    Query Match
    Best Local Similarity 29.2%; Score 214.5; DB 8; Length 4495; Pred. No. 3.7e-06;

RESULT 1324
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PN WO200310215-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
    Query Match
    Best Local Similarity 29.2%; Score 214.5; DB 6; Length 4495; Pred. No. 3.7e-06;

RESULT 1325
ID ADO08273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN US200401859-A1.
PD 29-JAN-2004.
PA (CURA-) CURAGEN CORP.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
    Query Match
    Best Local Similarity 13.9%; Score 214.5; DB 8; Length 4495; Pred. No. 3.7e-06;

RESULT 1326
ID ADK40856 standard; peptide; 42 AA.
DE Human FAM, Glu-C proteolytic fragment.
PN US6599688-B1.
PD 02-MAR-2004.
PA (UNYN) UNIV NEW YORK STATE RES FOUND.
    Query Match
    Best Local Similarity 97.6%; Score 214; DB 8; Length 42; Pred. No. 1.7e-08;

RESULT 1327
ID ADU66696 standard; peptide; 42 AA.
DE Human FAM endoproteinase GluC proteolytic peptide.
PN US200423576-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
    Query Match
    Best Local Similarity 13.9%; Score 214.5; DB 8; Length 42;

RESULT 1328
ID ABG03933 standard; protein; 1240 AA.
DE Novel human diagnostic protein #3924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSEQ INC.
    Query Match
    Best Local Similarity 97.6%; Score 213.5; DB 4; Length 1240; Pred. No. 1.7e-08;

RESULT 1329
ID AAB47771 standard; protein; 1336 AA.
DE Human thrombospondin protein, BTL.012.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
    Query Match
    Best Local Similarity 29.2%; Score 213.5; DB 5; Length 1336; Pred. No. 9.6e-07;

RESULT 1330
ID ADG39841 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #2.
PN US200320384-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
    Query Match
    Best Local Similarity 13.8%; Score 213.5; DB 7; Length 1708; Pred. No. 1.1e-06;

RESULT 1331
ID ADG39840 standard; protein; 1708 AA.
DE Protein similar to human NOV9 #1.
PN US200320384-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (TOPP/) TOPPER J N.
PA (MEHR/) MEHRABAN F.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
    Query Match
    Best Local Similarity 13.8%; Score 213.5; DB 7; Length 1708; Pred. No. 1.4e-06;

RESULT 1332
ID ABU12084 standard; protein; 1902 AA.
DE Human NOV25c CG56914-03 protein SEQ ID 88.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
    Query Match
    Best Local Similarity 13.8%; Score 213.5; DB 6; Length 1902; Pred. No. 1.4e-06;

RESULT 1333
ID ADH72108 standard; protein; 1902 AA.
DE Human protein of the invention NOV43d SEQ ID NO:1004.
PN WO200310215-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
    Query Match
    Best Local Similarity 29.2%; Score 213.5; DB 6; Length 1902; Pred. No. 1.6e-06;

RESULT 1334
Query Match   13.8%;   Score 213.5; DB 8; Length 1902;
Best Local Similarity   29.2%;   Pred. No. 1.6e-06;
ID   ADB16058 standard; protein; 1953 AA.
DE   G-coupled protein receptor related polypeptide, SEQ ID No 88.
PN   WO20028384l-A2.
PD   24-OCT-2002.
PA   (CURA-) CURAGEN CORP.
PA   (LILL/) LI L.
PA   (GERL/) GERLACH V.
PA   (LIUX/) LIU X.
PA   (MILL/) MILLER C E.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (ZHON/) ZHONG H.
PA   (SMIT/) SMITHSON G.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (VOSS/) VOSS E Z.
PA   (VERN/) VERNET C A.
PA   (MACD/) MACDOUGALL J R.
PA   (RAST/) RASTELLI L.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (MEZE/) MEZES P S.
PA   (FURT/) FURTAK K.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (MALY/) MALYANKAR U M.
PA   (SHIM/) SHIMKETS R A.
PA   (TAUP/) TAUPIER R J.
PA   (EDIN/) EDINGER S.
PA   (MAZU/) MAZUR A.

RESULT 1335
Query Match   13.8%;   Score 213.5; DB 7; Length 1953;
Best Local Similarity   29.2%;   Pred. No. 1.6e-06;
ID   ADL93997 standard; protein; 1953 AA.
DE   Human G-coupled protein receptor-related protein #44.
PN   US20040062O5-A1.
PD   08-JAN-2004.

RESULT 1336
Query Match   13.8%;   Score 213.5; DB 8; Length 3645;
Best Local Similarity   29.2%;   Pred. No. 1.6e-06;
ID   ADJ83136 standard; protein; 3645 AA.
DE   Human hemicentrin protein - SEQ ID 127.
PN   US20031706SO-Al.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.

PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.

RESULT 1337
Query Match   13.8%;   Score 213.5; DB 7; Length 3645;
Best Local Similarity   29.2%;   Pred. No. 3.4e-06;
ID   AEB94406 standard; protein; 5622 AA.
DE   Human hemicentin/FIBL-6 protein, SEQ ID NO: 128.
PN   US20051766O2-A1.
PD   11-AUG-2005.
PA   (UYMI-) UNIV MIAMI.

RESULT 1338
Query Match   13.8%;   Score 213.5; DB 7; Length 5622;
Best Local Similarity   29.2%;   Pred. No. 5.6e-06;
ID   ABP60991 standard; protein; 5635 AA.
DE   Novel human protein, SEQ ID 78.
PN   WO20025OlO5-Al.
PD   27-JUN-2002.
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
PA   (GLAX) GLAXO GROUP LTD.

RESULT 1339
Query Match   13.8%;   Score 213.5; DB 5; Length 5635;
Best Local Similarity   29.2%;   Pred. No. 5.6e-06;
ID   ADJ70089 standard; protein; 5636 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN   WO20030877GB-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.

RESULT 1340
Query Match   13.8%;   Score 213.5; DB 7; Length 5636;
Best Local Similarity   29.2%;   Pred. No. 5.6e-06;
ID   ADJ83137 standard; protein; 5636 AA.
DE   Human hemicentin protein - SEQ ID 128.
PN   US20031706SO-Al.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.

RESULT 1341
Query Match   13.8%;   Score 213.5; DB 8; Length 5636;
Best Local Similarity   29.2%;   Pred. No. 5.6e-06;
ID   ADK60205 standard; protein; 5636 AA.
DE   Angiogenesis differentially expressed protein GS-P29.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (ALMA/) AL MAHMOOD S.
PA   (GENE-) GENE SIGNAL.

RESULT 1342
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 13.8%; Score 213.5; DB 8; Length 5636;
Best Local Similarity 29.2%; Pred. No. 5.6e-06;

RESULT 1343
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 13.8%; Score 213.5; DB 8; Length 5636;
Best Local Similarity 29.2%; Pred. No. 5.6e-06;

RESULT 1344
ID ADY74314 standard; protein; 4126 AA.
DE Human hemicentin protein lacking part of the N-terminus.
PN US6867291-B1.
PD 15-MAR-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 13.8%; Score 212.5; DB 9; Length 4126;
Best Local Similarity 29.2%; Pred. No. 4.6e-06;

RESULT 1345
ID AEB34668 standard; protein; 4126 AA.
DE Human hemicentin protein, SEQ ID 4.
PN US20050164277-A1.
PD 28-JUL-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 13.8%; Score 212.5; DB 9; Length 4126;
Best Local Similarity 29.2%; Pred. No. 4.6e-06;

RESULT 1346
ID ADY74312 standard; protein; 5518 AA.
DE Human hemicentin protein.
PN US6867291-B1.
PD 15-MAR-2005.
PA (TURN/) TURNER C A.
PA (MATH/) MATHUR B.
PA (DONO/) DONOHO G.
Query Match 13.8%; Score 212.5; DB 9; Length 5518;
Best Local Similarity 29.2%; Pred. No. 6.5e-06;

RESULT 1347
ID AEB34666 standard; protein; 5518 AA.
DE Human hemicentin protein, SEQ ID 2.
PN US20050164277-A1.
PD 28-JUL-2005.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 13.8%; Score 212.5; DB 9; Length 5518;
Best Local Similarity 29.2%; Pred. No. 6.5e-06;

RESULT 1348
ID AAU18038 standard; protein; 294 AA.
DE Human immunoglobulin polypeptide SEQ ID No 183.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.6%; Score 210; DB 4; Length 294;
Best Local Similarity 26.3%; Pred. No. 3.2e-07;

RESULT 1349
ID ADB31662 standard; protein; 294 AA.
DE Human novel protein SEQ ID 183.
PN US20030077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.6%; Score 210; DB 7; Length 294;
Best Local Similarity 26.3%; Pred. No. 3.2e-07;

RESULT 1350
ID AAB08940 standard; protein; 245 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:97.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.5%; Score 208.5; DB 3; Length 245;
Best Local Similarity 30.4%; Pred. No. 3.4e-07;

RESULT 1351
ID AAB08926 standard; protein; 246 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:83.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.5%; Score 208.5; DB 3; Length 246;
Best Local Similarity 30.4%; Pred. No. 3.4e-07;

RESULT 1352
ID AAY72878 standard; protein; 352 AA.
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.
PN WO200116319-A2.
PD 08-MAR-2001.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1353
ID AAB50930 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH-) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1354
ID AAB65294 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:505.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1355
ID AAB84956 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:280.
PN WO200206690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 4; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1356
ID ABB95562 standard; protein; 352 AA.
DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 5; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

RESULT 1357
ID ADY31956 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN WO200193983-A1.
PD 13-DEC-2001.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 5; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1358
ID ABU58109 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027163-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1359
ID ABU59187 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2002132252-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1360
ID ABU82699 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003032023-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1361
ID ABU60618 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2002160384-A1.
PD 31-OCT-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1362
ID ABU08846 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003036635-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1363
ID ABU33812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003045687-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1364
ID ABU14000 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.

PA (GETH) GENENTECH LTD.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1365
ID ABU72585 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003003531-A1.
PD 02-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1366
ID ABG74762 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US200192752-A1.
PD 19-DEC-2002.

RESULT 1367
ID ABU59334 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2003027162-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1368
ID ABO26031 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002175576-A1.
PD 12-SEP-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1369
ID ABU82155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003080063-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1370
ID ABU59040 standard; protein; 352 AA.
DE Human secreted/transmembrane protein #177.
PN US2002142961-A1.
PD 03-OCT-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1371
ID ABU92418 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO3301.
PN US2003022187-A1.
PD 30-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1372
ID ABU59483 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003017476-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1373
ID ABU92249 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002123463-A1.
PD 05-SEP-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1374
ID ABU10955 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002177164-A1.
PD 28-NOV-2002.

PA (GETH) GENENTECH INC.
Query Match   13.4%; Score 207.5; DB 6; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;
RESULT 1375
ID ABU81707 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002171164-A1.

RESULT 1376
ID ABU88646 standard; protein; 352 AA.
DE Human secreted and transmembrane polypeptide PRO5723.
PN US2002197615-A1.
PD 26-DEC-2002.

RESULT 1377
ID   ABO34160 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003017981-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1378
ID   ABJ72335 standard; protein; 352 AA.
DE   Human PRO5723 protein.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1379
ID   ADA38016 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003054404-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1380
ID   ADA21702 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1381
ID   ADA10489 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein, PRO5723.
PN   US2003059831-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1382
ID   ADA18033 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1383
ID   ADA28141 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003054359-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1384
ID   ADA94721 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003059832-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1385
ID   ADA38946 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003059780-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1386
ID   ABJ72463 standard; protein; 352 AA.
DE   Human PRO5723 protein.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1387
ID   ADA93067 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003060407-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1388
ID   ABO34358 standard; protein; 352 AA.
DE   Human secreted/transmembrane polypeptide PRO 5723.
PN   US2003044933-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1389
ID   ABO53246 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003040473-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 6; Length 352;
Query Match 13.4%;

RESULT 1390
ID   ADA22628 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003044806-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1391
ID   ABO22616 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003049638-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1392
ID   ABO06794 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #141.
PN   US2003017982-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1393
ID   ABJ72165 standard; protein; 352 AA.
DE   Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1394
ID   ADA39487 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1395
ID   ADB83706 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003059782-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.7%;   Score 207.5; DB 7; Length 352;
Query Match 13.4%;

RESULT 1396
ID   ADB80812 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088068-A1.

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PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1397
ID   ADB73353 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030096968-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1398
ID   ADB96513 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US20030054403-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1399
ID   ADB78435 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1400
ID   ADB85083 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1401
ID   ADB78189 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030092886-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1402
ID   ADB87255 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1403
ID   ADB84837 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1404
ID   ADB83952 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1405
ID   ADB73107 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030092887-A1.
PD   15-MAY-2003.


     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
PN   US20030027754-A1.
PD   06-FEB-2003.
RESULT 1406
ID   ADC57985 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US20030045463-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1407
ID   ADC55349 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US20030049681-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1408
ID   ADC12216 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US20030064375-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1409
ID   ADC56638 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US20030069403-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1410
ID   ADC11683 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US20030069403-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1411
ID   ADC36945 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1412
ID   ADC21935 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030099969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1413
ID   ADC49966 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1414
ID   ADC49165 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              13.4%;   Score 207.5;   DB 7;   Length 352;
     Best Local Similarity    26.7%;   Pred. No. 6.1e-07;
RESULT 1415
ID   ADC49682 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030088071-A1.
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1416
ID ADC47543 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200308072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1417
ID ADC14805 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200308546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1418
ID ADC47288 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305288-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1419
ID ADC82162 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US200308623-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1420
ID ADD08337 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200303461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1421
ID ADD07804 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200219299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1422
ID ADC78163 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200309672-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1423
ID ADC82695 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US200373816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1424
ID ADD06398 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1425
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

ID ADD10569 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US200305011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1427
ID ADC77917 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200308066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1428
ID ADD07124 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1429
ID ADD11529 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US200193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1430
ID ADC83371 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US200309783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1431
ID ADD50880 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1432
ID ADD15380 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305437-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1433
ID ADD51126 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200305290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.4%; Score 207.5; DB 7; Length 352;
Best Local Similarity 26.7%; Pred. No. 6.1e-07;

RESULT 1434
ID ADD55478 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US200307593-A1.

RESULT 1435
ID   ADD37322 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US200310012-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1436
ID   ADD56436 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US200305012-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1437
ID   ADD54874 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US200307594-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1438
ID   ADD50607 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200309971-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1439
ID   ADD50361 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200309970-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1440
ID   ADD51372 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US200305289-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1441
ID   ADD31893 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US200306647-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1442
ID   ADE27028 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200307304-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1443
ID   ADE26495 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200307305-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1444
ID   ADF67432 standard; protein; 352 AA.
DE   Human PRO5723 amino acid sequence SEQ ID NO:505.
PN   US200219148-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1445
ID   ADE94085 standard; protein; 352 AA.
DE   Immune disease treatment/diagnosis related PRO5723.
PN   US200308199-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1446
ID   ADI35686 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US200305045 7-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1447
ID   ADI00179 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200304682-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 7;   Length 352;

RESULT 1448
ID   ADC48919 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200309288 8-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 8;   Length 352;

RESULT 1449
ID   ADE21090 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200310073 5-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 8;   Length 352;

RESULT 1450
ID   ADE05934 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200310072 8-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 8;   Length 352;

RESULT 1451
ID   ADD75163 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200310071 7-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 8;   Length 352;

RESULT 1452
ID   ADD75909 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200310071 2-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   13.4%;
                        26.7%;   Score 207.5;   DB 8;   Length 352;

RESULT 1453
ID   ADD85141 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200310072 2-A1.
PD   29-MAY-2003.

RESULT 1454
ID   ADD86967 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1455
ID   ADE20844 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1456
ID   ADE39141 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030963622-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1457
ID   ADE05688 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1458
ID   ADD73673 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1459
ID   ADD78513 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1460
ID   ADE41530 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1461
ID   ADE21336 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US200310736-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1462
ID   ADD77451 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 1463
ID   ADE20598 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1464
ID   ADD75663 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US200310064-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1465
ID   ADD74179 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1466
ID   ADD74425 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1467
ID   ADD76155 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1468
ID   ADD85647 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1469
ID   ADE05196 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1470
ID   ADD75409 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

RESULT 1471
ID   ADD76953 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   13.4%;   26.7%;   Score 207.5;   Pred. No. 6.1e-07;   DB 8;   Length 352;

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Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1472
ID   ADB86721 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1473
ID   ADD78189 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1474
ID   ADD77697 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1475
ID   ADD77943 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1476
ID   ADD85401 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1477
ID   ADD73933 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1478
ID   ADD74671 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1479
ID   ADD77199 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1480
ID   ADD85893 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;


RESULT 1481
ID   ADE05442 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1482
ID   ADD74917 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide #108.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1483
ID   ADF35631 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1484
ID   ADG11881 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1485
ID   ADG05729 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1486
ID   ADG27283 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1487
ID   ADG11346 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1488
ID   ADG12125 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1489
ID   ADF94682 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1490
ID   ADG06778 standard; protein; 352 AA.
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DE   Human PRO polypeptide #108.
PN   US20030969966-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1491
ID   ADH39122 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030965965-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1492
ID   ADH19751 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US20030228656-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1493
ID   ADH21244 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US20030224358-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1494
ID   ADH20084 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US20030219856-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1495
ID   ADH43713 standard; protein; 352 AA.
DE   Human PRO polypeptide #140.
PN   US20030224984-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1496
ID   ADG34212 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20040006206-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1497
ID   ADI33682 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20030969960-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1498
ID   ADH69776 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US20040019183-A1.
PD   29-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1499
ID   ADI29937 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030969961-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

RESULT 1500
ID   ADM27334 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20040044179-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   13.4%;   Score 207.5;   DB 8;   Length 352;
Best Local Similarity   26.7%;   Pred. No. 6.1e-07;

OM protein - protein search, using sw model

GenCore version 5.1.8
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Run on: May 16, 2006, 07:01:24 ; Search time 47 Seconds
(without alignments)
525.958 Million cell updates/sec

Title: US-10-785-433-1
Perfect score: 1544
Sequence: 1 MGTKAQVERKLCLFLIAIL...........YSQPSARSEGEFKQTSSFLV 299

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
  1: /cgn_2_6/ptodata/1/iaa/5_COMB.pep:*
  2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
  3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
  4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
  5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1544	100.0	299	2	US-09-188-930-331	Sequence 331, App
2	1544	100.0	299	2	US-09-462-270-2	Sequence 2, Appli
3	1544	100.0	299	2	US-09-254-465A-1	Sequence 1, Appli
4	1544	100.0	299	2	US-09-312-283C-189	Sequence 189, App
5	1544	100.0	299	2	US-09-312-283C-331	Sequence 331, App
6	1544	100.0	299	2	US-09-907-794A-119	Sequence 119, App
7	1544	100.0	299	2	US-09-905-125A-119	Sequence 119, App
8	1544	100.0	299	2	US-09-902-775A-119	Sequence 119, App
9	1544	100.0	299	2	US-09-397-243D-3	Sequence 3, Appli
10	1544	100.0	299	2	US-09-906-700-119	Sequence 119, App
11	1544	100.0	299	2	US-09-903-603A-119	Sequence 119, App
12	1544	100.0	299	2	US-09-904-920A-119	Sequence 119, App
13	1544	100.0	299	2	US-09-909-064-119	Sequence 119, App
14	1544	100.0	299	2	US-09-905-381A-119	Sequence 119, App
15	1544	100.0	299	2	US-09-906-618-119	Sequence 119, App
16	1544	100.0	299	2	US-09-953-499-1	Sequence 1, Appli
17	1544	100.0	299	2	US-09-906-646-119	Sequence 119, App
18	1544	100.0	299	2	US-09-904-462-119	Sequence 119, App
19	1544	100.0	299	2	US-09-902-736A-119	Sequence 119, App
20	1544	100.0	299	2	US-09-906-722A-119	Sequence 119, App
21	1532	99.2	299	2	US-09-188-930-189	Sequence 189, App
22	1372	88.9	263	2	US-09-254-465A-25	Sequence 25, Appl
23	1372	88.9	263	2	US-09-953-499-25	Sequence 25, Appl
24	1355	87.8	260	2	US-09-254-465A-23	Sequence 23, Appl
25	1355	87.8	260	2	US-09-953-499-23	Sequence 23, Appl
26	1073.5	69.5	300	2	US-09-254-465A-10	Sequence 10, Appl
27	1073.5	69.5	300	2	US-09-397-243D-12	Sequence 12, Appl
28	1073.5	69.5	300	2	US-09-953-499-10	Sequence 10, Appl
29	1042.5	67.5	205	2	US-09-462-270-4	Sequence 4, Appli
30	910	58.9	193	2	US-09-397-243D-4	Sequence 4, Appl
31	576	37.3	134	2	US-09-312-283C-173	Sequence 173, App
32	569	36.9	173	2	US-09-188-930-173	Sequence 173, App
33	429	27.8	298	2	US-09-152-060-76	Sequence 76, Appl
34	429	27.8	298	2	US-09-852-797-76	Sequence 76, Appl
35	429	27.8	298	2	US-09-853-161-76	Sequence 76, Appl
36	424	27.5	424	2	US-10-058-993-76	Sequence 76, Appl
37	424	27.5	310	2	US-09-907-794A-423	Sequence 423, App
38	424	27.5	310	2	US-09-905-125A-423	Sequence 423, App
39	424	27.5	310	2	US-09-906-700-423	Sequence 423, App
40	424	27.5	310	2	US-09-903-603A-423	Sequence 423, App
41	424	27.5	310	2	US-09-904-920A-423	Sequence 423, App
42	424	27.5	310	2	US-09-909-064-423	Sequence 423, App
43	424	27.5	310	2	US-09-905-381A-423	Sequence 423, App
44	424	27.5	310	2	US-09-906-618-423	Sequence 423, App
45	424	27.5	310	2	US-09-906-646-423	Sequence 423, App
46	424	27.5	310	2	US-09-904-462-423	Sequence 423, App
47	424	27.5	310	2	US-09-902-736A-423	Sequence 423, App
48	424	27.5	310	2	US-09-906-722A-423	Sequence 423, App
49	424	27.5	310	2	US-10-033-301-20	Sequence 20, Appl
50	412	26.7	76	2	US-09-397-243D-9	Sequence 9, Appli
51	409	26.5	76	2	US-08-597-495B-9	Sequence 9, Appli
52	404	26.2	312	2	US-09-397-243D-11	Sequence 11, Appl
53	404	26.2	312	2	US-09-068-051A-9	Sequence 9, Appli
54	404	26.2	312	2	US-09-907-794A-64	Sequence 64, Appl
55	404	26.2	312	2	US-09-905-125A-64	Sequence 64, Appl
56	404	26.2	312	2	US-09-902-775A-64	Sequence 64, Appl
57	404	26.2	312	2	US-09-906-700-64	Sequence 64, Appl
58	404	26.2	312	2	US-09-903-603A-64	Sequence 64, Appl
59	404	26.2	312	2	US-09-904-920A-64	Sequence 64, Appl
60	404	26.2	312	2	US-09-909-064-64	Sequence 64, Appl
61	404	26.2	312	2	US-09-905-381A-64	Sequence 64, Appl
62	404	26.2	312	2	US-09-906-618-64	Sequence 64, Appl
63	404	26.2	312	2	US-09-906-646-64	Sequence 64, Appl
64	404	26.2	312	2	US-09-904-462-64	Sequence 64, Appl
65	404	26.2	312	2	US-09-902-736A-64	Sequence 64, Appl
66	404	26.2	312	2	US-09-906-722A-64	Sequence 64, Appl
67	404	26.2	312	2	US-10-033-301-64	Sequence 64, Appl
68	281.5	18.2	318	2	US-09-068-051A-32	Sequence 32, Appl
69	279	18.1	316	1	US-08-597-495B-22	Sequence 13, Appl
70	272.5	17.6	319	2	US-09-397-243D-13	Sequence 22, Appl
71	272.5	17.6	319	2	US-09-068-051A-22	Sequence 22, Appl
72	272.5	17.6	319	2	US-09-336-536-67	Sequence 67, Appl
73	272.5	17.6	319	2	US-09-254-465A-6	Sequence 6, Appli
74	272.5	17.6	319	2	US-09-953-499-6	Sequence 6, Appli
75	273	17.6	273	2	US-09-254-465A-26	Sequence 26, Appl
76	272	17.6	272	2	US-09-953-499-26	Sequence 26, Appl
77	270	17.4	270	2	US-09-254-455A-24	Sequence 24, Appl
78	270	17.4	270	2	US-09-953-499-24	Sequence 24, Appl
79	227	14.7	42	2	US-09-397-243D-6	Sequence 6, Appli
80	227	14.7	50	2	US-08-342-449-11	Sequence 11, Appl
81	214	13.9	42	2	US-09-397-243D-15	Sequence 15, Appl
82	212.5	13.8	4126	1	US-08-597-495B-3	Sequence 3, Appli
83	212.5	13.8	5518	2	US-09-272-496-2	Sequence 2, Appli
84	207.5	13.4	352	2	US-09-991-181-505	Sequence 505, Ap
85	207.5	13.4	352	2	US-09-990-444-505	Sequence 505, App
86	207.5	13.4	352	2	US-09-997-333-505	Sequence 505, App
87	207.5	13.4	365	2	US-09-949-016-6064	Sequence 6064, Ap
88	207.5	13.4	365	2	US-09-949-016-11050	Sequence 11050, A
89	207.5	13.4	365	2	US-08-928-393B-2	Sequence 2, Appli
90	207.5	13.4	383	2	US-09-324-541-2	Sequence 2, Appli
91	207.5	13.4	365	2	US-09-910-174B-28	Sequence 28, Appl
92	203.5	13.2	365	2	US-09-620-461-28	Sequence 28, Appl
93	203	13.1	365	2	US-08-175-928-2	Sequence 2, Appli
94	202	13.1	315	2	US-09-899-634C-4	Sequence 4, Appli
95	202	13.1	315	2	US-09-899-634C-2	Sequence 28, Appl
96	201	13.0	387	2	US-09-620-461-28	Sequence 2, Appli
97	197	12.8	365	2	US-09-175-928-2	Sequence 2, Appli
98	196	12.7	261	2	US-09-899-634C-4	Sequence 4, Appli
99	196	12.7	373	2	US-09-991-181-503	Sequence 503, App
100	196	12.7	373	2	US-09-999-833A-59	Sequence 59, Appl

No.					Reference	Sequence
101	196	12.7	373	2	US-09-990-444-503	Sequence 503, App
102	196	12.7	373	2	US-09-997-333-503	Sequence 503, Appl
103	196	12.7	373	2	US-09-992-598-503	Sequence 503, App
104	196	12.7	373	2	US-10-020-445A-59	Sequence 59, Appl
105	194	12.7	373	2	US-08-928-383B-23	Sequence 23, Appl
106	194	12.6	365	2	US-08-928-383B-24	Sequence 24, Appl
107	189	12.6	365	2	US-09-953-499-2	Sequence 2, Appl
108	182	12.2	329	2	US-08-928-383B-26	Sequence 26, Appl
109	181	11.8	329	2	US-10-104-047-3709	Sequence 3709, Ap
110	181	11.7	1101	2	US-08-986-485-2	Sequence 2, Appli
111	180.5	11.7	316	2	US-09-999-833A-137	Sequence 137, App
112	179	11.6	340	2	US-09-651-200-2	Sequence 2, Appli
113	179	11.6	441	2	US-09-651-200-4	Sequence 4, Appli
114	179	11.6	534	2	US-09-651-200-6	Sequence 6, Appli
115	179	11.6	534	2	US-09-651-200-24	Sequence 24, Appli
116	178.5	11.6	316	2	US-09-910-174B-24	Sequence 24, Appli
117	178.5	11.6	316	2	US-09-620-461-24	Sequence 24, Appli
118	178.5	11.6	321	2	US-09-915-789A-1	Sequence 1, Appli
119	178.5	11.6	321	2	US-09-254-465A-2	Sequence 2, Appli
120	178.5	11.6	321	2	US-09-999-833A-52	Sequence 52, Appli
121	178.5	11.6	321	2	US-09-999-833A-52	Sequence 52, Appl
122	178.5	11.6	321	2	US-10-020-445A-52	Sequence 52, Appl
123	178.5	11.6	501	1	US-08-408-095-31	Sequence 31, Appl
124	178.5	11.6	501	2	US-09-949-002-328	Sequence 328, Appl
125	177.5	11.5	847	2	US-09-979-424-1	Sequence 427, App
126	176	11.5	862	1	US-08-979-424-1	Sequence 1, Appli
127	176	11.4	390	2	US-09-907-794A-39	Sequence 39, Appli
128	176	11.4	390	2	US-09-905-125A-39	Sequence 39, Appli
129	176	11.4	390	2	US-09-902-775A-39	Sequence 39, Appli
130	176	11.4	390	2	US-09-906-700-39	Sequence 39, Appli
131	176	11.4	390	2	US-09-903-603A-39	Sequence 39, Appli
132	176	11.4	390	2	US-09-904-920A-39	Sequence 39, Appli
133	176	11.4	390	2	US-09-999-064-39	Sequence 39, Appli
134	176	11.4	390	2	US-09-905-381A-39	Sequence 39, Appli
135	176	11.4	390	2	US-09-906-618-39	Sequence 39, Appli
136	176	11.4	390	2	US-09-906-646-39	Sequence 39, Appli
137	176	11.4	390	2	US-09-904-462-39	Sequence 39, Appli
138	176	11.4	390	2	US-09-902-736A-39	Sequence 39, Appli
139	176	11.4	390	2	US-09-906-722A-39	Sequence 39, Appli
140	176	11.3	398	2	US-09-778-510-6	Sequence 6, Appli
141	174	11.3	398	2	US-09-907-794A-84	Sequence 84, Appli
142	174	11.3	398	2	US-09-905-125A-84	Sequence 84, Appli
143	174	11.3	398	2	US-09-902-775A-84	Sequence 84, Appli
144	174	11.3	398	2	US-09-906-700-84	Sequence 84, Appli
145	174	11.3	398	2	US-09-903-603A-84	Sequence 84, Appli
146	174	11.3	398	2	US-09-904-920A-84	Sequence 84, Appli
147	174	11.3	398	2	US-09-999-064-84	Sequence 84, Appli
148	174	11.3	398	2	US-09-905-381A-84	Sequence 84, Appli
149	174	11.3	398	2	US-09-906-618-84	Sequence 84, Appli
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151	174	11.3	398	2	US-09-904-462-84	Sequence 84, Appli
152	174	11.3	398	2	US-09-902-736A-84	Sequence 84, Appli
153	174	11.3	398	2	US-09-906-722A-84	Sequence 84, Appli
154	174	11.3	432	2	US-09-903-603A-84	Sequence 84, Appli
155	173.5	11.2	316	2	US-09-778-510-2	Sequence 2, Appli
156	173.5	11.2	1395	2	US-09-540-245A-15	Sequence 15, Appli
157	173.5	11.2	1395	2	US-10-289-776-15	Sequence 15, Appli
158	173	11.2	1709	2	US-09-949-016-10503	Sequence 10503, A
159	172.5	11.2	341	2	US-09-336-536-29	Sequence 29, Appl
160	172.5	11.2	370	1	US-09-336-536-28	Sequence 28, Appl
161	172	11.2	650	2	US-10-047-047-3395	Sequence 3395, Ap
162	171	11.2	316	2	US-09-907-794A-290	Sequence 290, App
163	171	11.1	1059	2	US-09-905-125A-290	Sequence 290, App
164	171	11.1	1059	2	US-09-902-775A-290	Sequence 290, App
165	171	11.1	1059	2	US-09-906-700-290	Sequence 290, App
166	171	11.1	1059	2	US-09-903-603A-290	Sequence 290, App
167	171	11.1	1059	2	US-09-904-920A-290	Sequence 290, App
168	171	11.1	1059	2	US-09-999-064-290	Sequence 290, App
169	171	11.1	1059	2	US-09-905-381A-290	Sequence 290, App
170	171	11.1	1059	2	US-09-906-618-290	Sequence 290, App
171	171	11.1	1059	2	US-09-906-646-290	Sequence 290, App
172	171	11.1	1059	2	US-09-904-462-290	Sequence 290, App
173	171	11.1	1059	2	US-09-902-736A-290	Sequence 290, App

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174	171	11.1	1059	2	US-09-906-722A-290	Sequence 290, App
175	171	11.1	1091	2	US-08-986-485-5	Sequence 290, Appli
176	171	11.1	1119	2	US-09-907-794A-294	Sequence 294, Appl
177	171	11.1	1119	2	US-09-905-125A-294	Sequence 294, Appl
178	171	11.1	1119	2	US-09-778-510-4	Sequence 294, Appl
179	171	11.1	1119	2	US-10-104-047-3036	Sequence 3036, Ap
180	171	11.1	1119	2	US-09-902-775A-294	Sequence 294, Appl
181	171	11.1	1119	2	US-09-906-700-294	Sequence 294, App
182	171	11.1	1119	2	US-09-903-603A-294	Sequence 294, App
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184	171	11.1	1119	2	US-09-904-920A-294	Sequence 294, App
185	171	11.1	1119	2	US-09-999-064-294	Sequence 294, App
186	171	11.1	1119	2	US-09-905-381A-294	Sequence 294, App
187	171	11.1	1119	2	US-09-906-618-294	Sequence 294, App
188	171	11.1	398	2	US-09-906-646-294	Sequence 294, App
189	168.5	10.9	466	2	US-09-904-462-294	Sequence 294, App
190	168	10.9	317	2	US-10-104-047-306	Sequence 3036, Ap
191	167.5	10.8	615	2	US-09-604-107A-8	Sequence 8, Appli
192	167.5	10.8	615	1	US-08-752-307B-9	Sequence 3036, Ap
193	167.5	10.8	615	1	US-09-707-802-8	Sequence 8, Appli
194	167.5	10.8	615	2	US-09-906-722A-294	Sequence 9, Appli
195	167.5	10.8	1297	2	US-09-540-245A-17	Sequence 17, Appl
196	167.5	10.8	1297	2	US-10-289-776-17	Sequence 17, Appl
197	167	10.8	1571	2	US-08-956-991-11	Sequence 11, Appl
198	166.5	10.8	1910	2	US-08-956-991-2	Sequence 2, Appli
199	166.5	10.8	394	2	US-09-336-536-39	Sequence 39, Appl
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202	160.5	10.4	365	2	US-09-336-536-40	Sequence 40, Appl
203	160.5	10.4	2596	2	US-09-548-473B-6	Sequence 6, Appli
204	158	10.2	607	1	US-08-752-307B-12	Sequence 12, Appl
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206	158	10.2	607	1	US-09-707-802-12	Sequence 12, Appl
207	157.5	10.2	837	2	US-09-991-326-12	Sequence 12, Appl
208	157	10.2	313	2	US-09-949-016-6515	Sequence 6515, Ap
209	157	10.2	344	2	US-09-700-397-4	Sequence 3, Appli
210	157	10.2	344	2	US-09-700-397-3	Sequence 3, Appli
211	156	10.1	894	2	US-10-020-445A-523	Sequence 523, App
212	155.5	10.1	819	2	US-09-999-833A-523	Sequence 523, App
213	154.5	10.0	344	2	US-09-949-016-10605	Sequence 10605, A
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216	154.5	10.0	462	2	US-09-707-802-7	Sequence 7, Appli
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222	154	10.0	1070	1	US-09-787-443-44	Sequence 44, Appl
223	153.5	9.9	828	2	US-09-961-403-3	Sequence 3, Appli
224	153	9.9	780	1	US-08-261-304-2	Sequence 2, Appli
225	153	9.9	780	1	US-08-232-538-14	Sequence 14, Appl
226	153	9.9	780	1	US-08-786-164-14	Sequence 14, Appl
227	153	9.9	1338	2	US-08-752-307B-21	Sequence 21, Appl
228	152	9.9	1338	1	US-08-506-296B-21	Sequence 5, Appli
229	152	9.8	304	1	US-08-750-141A-3	Sequence 3, Appli
230	152	9.8	325	1	US-08-414-657D-44	Sequence 44, Appl
231	152	9.8	325	1	US-09-119-014D-2	Sequence 21, Appl
232	152	9.8	325	1	US-09-135-080-2	Sequence 2, Appli
233	152	9.8	338	1	US-08-414-657D-60	Sequence 8, Appli
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236	152	9.8	891	2	US-09-345-473E-25	Sequence 25, Appl
237	152	9.8	891	2	US-09-862-027-25	Sequence 25, Appl
238	152	9.8	1115	2	US-10-012-231A-58	Sequence 58, Appl
239	152	9.8	1115	2	US-10-015-389A-58	Sequence 58, Appl
240	152	9.8	1115	2	US-10-006-768A-58	Sequence 58, Appl
241	152	9.8	1115	2	US-10-015-671A-58	Sequence 58, Appl
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244	152	9.8	1115	2	US-10-006-041A-58	Sequence 58, Appl
245	152	9.8	1115	2	US-10-012-064A-58	Sequence 58, Appl
246	152	9.8	1253	2	US-08-506-296B-14	Sequence 14, Appl

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247	150.5	9.7	349	2	US-09-924-103-4	Sequence 4, Appli
248	150.5	9.7	1501	1	US-08-447-464-3	Sequence 3, Appli
249	150.5	9.7	1501	1	US-08-716-679-3	Sequence 3, Appli
250	150	9.7	642	1	US-08-217-299-1	Sequence 1, Appli
251	150	9.7	698	2	US-08-602-725-36	Sequence 36, Appli
252	150	9.7	702	2	US-09-949-016-6484	Sequence 6484, Ap
253	150	9.7	734	1	US-08-389-459A-17	Sequence 17, Appl
254	150	9.7	734	1	US-08-987-867A-17	Sequence 17, Ap
255	149	9.7	740	2	US-09-949-016-8168	Sequence 8168, Ap
256	149	9.7	450	2	US-09-907-794A-320	Sequence 320, App
257	149	9.7	450	2	US-09-905-125A-320	Sequence 320, App
258	149	9.7	450	2	US-09-902-775A-320	Sequence 320, App
259	149	9.7	450	2	US-09-906-700-320	Sequence 320, App
260	149	9.7	450	2	US-09-906-618-320	Sequence 320, App
261	149	9.7	450	2	US-09-903-603A-320	Sequence 320, App
262	149	9.7	450	2	US-09-904-920A-320	Sequence 320, App
263	149	9.7	450	2	US-09-909-064-320	Sequence 320, App
264	149	9.7	450	2	US-09-905-381A-320	Sequence 320, App
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266	149	9.7	450	2	US-09-904-462-320	Sequence 320, App
267	149	9.7	450	2	US-09-902-736A-320	Sequence 320, App
268	149	9.7	450	2	US-09-906-722A-320	Sequence 320, App
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270	149	9.7	647	4	PCT-US93-00031-21	Sequence 21, Appl
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273	149	9.7	647	4	PCT-US93-00031-11	Sequence 11, Appl
274	149	9.7	647	4	PCT-US93-00031-23	Sequence 23, Appl
275	149	9.7	735	4	PCT-US93-00031-13	Sequence 13, Appl
276	149	9.7	736	4	PCT-US93-00031-15	Sequence 15, Appl
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278	149	9.7	739	4	PCT-US93-00031-9	Sequence 9, Appli
279	149	9.7	739	4	PCT-US93-00031-17	Sequence 17, Appl
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282	148.5	9.6	1311	2	US-08-340-011-5	Sequence 5, Appli
283	148.5	9.6	1311	2	US-08-901-710-5	Sequence 5, Appli
284	148.5	9.6	1311	2	US-09-169-079-5	Sequence 5, Appli
285	148.5	9.6	1021	2	US-08-497-025-3	Sequence 3, Appli
286	148	9.6	1021	2	US-09-949-002-363	Sequence 363, App
287	148	9.6	227	2	US-10-004-860-947	Sequence 947, App
288	148	9.6	227	2	US-09-205-258-947	Sequence 947, App
289	147.5	9.6	246	2	US-09-336-536-31	Sequence 31, Appl
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291	147.5	9.6	662	2	US-08-261-304-7	Sequence 7, Appli
292	147.5	9.6	946	4	PCT-US95-08493-13	Sequence 13, Appl
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294	146.5	9.5	308	1	US-08-414-657D-46	Sequence 46, Appl
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299	146	9.5	4391	2	US-09-915-789A-20	Sequence 20, Appl
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302	145.5	9.4	1194	2	US-08-874-678-1	Sequence 1, Appli
303	145.5	9.4	758	2	US-08-643-839-1	Sequence 1, Appli
304	145	9.4	758	2	US-09-051-363-24	Sequence 24, Appl
305	145	9.4	758	2	US-09-348-886-1	Sequence 1, Appli
306	145	9.4	758	2	US-10-105-901A-1	Sequence 1, Appli
307	145	9.4	802	2	US-09-173-151A-33	Sequence 33, Appl
308	145	9.4	306	2	US-10-191-029-12	Sequence 12, Appl
309	144.5	9.4	478	4	PCT-US95-08493-15	Sequence 15, Appl
310	144	9.3	860	4	PCT-US95-08493-19	Sequence 19, Appl
311	144	9.3	868	4	PCT-US95-08493-21	Sequence 21, Appl
312	144	9.3	1381	2	US-09-540-245A-16	Sequence 16, Appl
313	144	9.3	1381	2	US-10-289-776-16	Sequence 16, Appl
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318	143.5	9.3	444	1	US-08-659-984A-5	Sequence 5, Appli
319	143.5	9.3	444	2	US-08-660-531-5	Sequence 5, Appli
320	143.5	9.3	444	2	US-09-404-578-5	Sequence 5, Appli
321	143.5	9.3	504	2	US-09-949-016-7020	Sequence 7020, Ap
322	143.5	9.3	504	2	US-09-991-181-119	Sequence 119, App
323	143.5	9.3	504	2	US-09-990-444-119	Sequence 119, App
324	143.5	9.3	504	2	US-09-997-333-119	Sequence 119, App
325	143.5	9.3	504	1	US-09-992-598-119	Sequence 119, App
326	143.5	9.3	511	2	US-09-949-016-10054	Sequence 10054, A
327	143.5	9.3	310	1	US-09-949-016-7045	Sequence 7045, Ap
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332	143	9.3	1911	2	US-08-800-825A-5	Sequence 5, Appli
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334	142.5	9.2	289	2	US-08-842-248A-12	Sequence 12, Appl
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343	141.5	9.2	337	1	US-09-560-639-6	Sequence 6, Appli
344	141.5	9.2	337	1	US-08-441-893A-18	Sequence 18, Appl
345	141.5	9.2	337	1	US-09-032-331-41	Sequence 41, Appl
346	141.5	9.2	342	2	US-09-560-639-7	Sequence 7, Appli
347	141.5	9.2	567	2	US-09-173-151A-24	Sequence 24, Appl
348	141.5	9.2	567	2	US-09-032-333-39	Sequence 39, Appl
349	141.5	9.2	567	2	US-09-949-016-6213	Sequence 6213, Ap
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354	141	9.1	868	1	US-09-077-955-1	Sequence 1, Appli
355	141	9.1	868	2	US-10-016-283-1	Sequence 1, Appli
356	141	9.1	1024	2	US-09-976-594-531	Sequence 531, App
357	141	9.1	1461	2	US-08-949-002-523	Sequence 523, App
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361	140	9.1	890	1	US-08-445-461-2	Sequence 2, Appli
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368	140	9.1	911	2	US-08-441-104A-1	Sequence 1, Appli
369	139	9.0	869	2	US-09-715-249-8	Sequence 8, Appli
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371	139	9.0	869	2	US-08-374-834A-16	Sequence 16, Appl
372	139	9.0	890	2	US-09-223-490-2	Sequence 2, Appli
373	138.5	9.0	911	2	US-09-077-955-33	Sequence 33, Appl
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390	138	8.9	1018	2	US-09-452-052-2	Sequence 2, Appli
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393	136.5	8.8	191	2	US-09-270-767-33678	Sequence 33678, A
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396	136.5	8.8	434	2	US-10-289-776-19	Sequence 19, Appl
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398	136.5	8.8	1180	2	US-09-949-016-6577	Sequence 6577, Ap
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407	135.5	8.8	1367	1	US-07-977-451-6	Sequence 6, Appli
408	135.5	8.8	1367	2	US-07-946-507-4	Sequence 4, Appli
409	135.5	8.8	1367	1	US-08-252-517-6	Sequence 6, Appli
410	135.5	8.8	1367	1	US-08-601-891-6	Sequence 6, Appli
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412	135.5	8.8	1367	1	US-09-021-324-6	Sequence 6, Appli
413	135.5	8.8	1367	1	US-08-193-829B-2	Sequence 2, Appl
414	135.5	8.8	1367	2	US-09-872-136B-6	Sequence 6, Appl
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420	135.5	8.8	1367	4	PCT-US92-09893-6	Sequence 6, Appl
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430	134.5	8.7	306	2	US-09-206-132-8	Sequence 8, Appli
431	134.5	8.7	306	2	US-09-425-516-31	Sequence 31, Appl
432	134	8.7	306	2	US-09-206-132-8	Sequence 8, Appli
433	134	8.7	640	2	US-09-949-016-7565	Sequence 7565, Ap
434	133.5	8.6	398	2	US-08-189-035-6	Sequence 6, Appli
435	133.5	8.6	398	2	US-09-382-086-6	Sequence 6, Appli
436	133.5	8.6	398	1	US-08-999-689A-5	Sequence 5, Appli
437	133.5	8.6	419	6	5169835-2	Patent No. 5169835
438	133.5	8.6	661	1	US-08-232-538-12	Sequence 12, Appl
439	133.5	8.6	661	1	US-08-786-164-12	Sequence 12, Appl
440	133.5	8.6	687	1	US-08-232-538-6	Sequence 6, Appli
441	133.5	8.6	687	1	US-08-786-164-6	Sequence 6, Appli
442	133.5	8.6	687	2	US-09-427-353-2	Sequence 2, Appli
443	132	8.5	352	2	US-09-999-833A-612	Sequence 612, App
444	132	8.5	352	2	US-10-020-445A-612	Sequence 612, App
445	132	8.5	1018	1	US-08-408-093-6	Sequence 6, Appli
446	132	8.5	1018	1	US-08-408-420A-6	Sequence 6, Appli
447	132	8.5	1018	1	US-08-714-901-6	Sequence 6, Appli
448	132	8.5	1018	2	US-08-040-741-6	Sequence 6, Appli
449	132	8.5	1044	2	US-09-949-016-10321	Sequence 10321, A
450	132	8.5	281	2	US-09-423-439-44	Sequence 44, Appl
451	131.5	8.5	816	1	US-07-640-029-1	Sequence 1, Appli
452	131.5	8.5	1266	1	US-08-506-296B-4	Sequence 4, Appli
453	130.5	8.5	729	1	US-07-640-029-3	Sequence 3, Appli
454	130.5	8.5	729	2	US-09-383-586-31	Sequence 31, Appl
455	130	8.5	529	2	US-09-823-038A-31	Sequence 31, Appl
456	129.5	8.4	212	2	US-08-205-697A-17	Sequence 17, Appl
457	129.5	8.4	306	2	US-08-205-697A-17	Sequence 17, Appl
458	129.5	8.4	306	2	US-08-702-525-17	Sequence 17, Appl
459	129.5	8.4	306	2	US-09-651-200-17	Sequence 17, Appl
460	129.5	8.4	306	2	US-09-667-135-35	Sequence 35, Appl
461	129.5	8.4	306	2	US-09-837-867A-17	Sequence 17, Appl
462	129.5	8.4	306	4	PCT-US95-02576-17	Sequence 17, Appl
463	129.5	8.4	417	2	US-09-949-016-6729	Sequence 6729, Ap
464	129.5	8.4	439	2	US-09-383-586-32	Sequence 32, Appl
465	129.5	8.4	439	2	US-09-823-038A-32	Sequence 32, Appl

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469	129.5	8.4	609	2	US-09-949-016-7749	Sequence 7749, Ap
470	129.5	8.4	609	2	US-09-949-016-7750	Sequence 7750, Ap
471	129.5	8.4	609	2	US-09-949-016-7751	Sequence 7751, Ap
472	129.5	8.4	609	2	US-09-949-016-7752	Sequence 7752, Ap
473	129.5	8.4	609	1	US-09-949-016-7753	Sequence 7753, Ap
474	129.5	8.4	609	2	US-09-949-016-7754	Sequence 7754, Ap
475	129.5	8.4	731	1	US-07-921-807B-7	Sequence 7, Appl
476	129.5	8.4	731	2	US-08-439-992A-5	Sequence 5, Appl
477	129.5	8.4	731	2	US-08-441-944A-3	Sequence 3, Appl
478	129.5	8.4	731	2	US-09-620-561-3	Sequence 3, Appl
479	129.5	8.4	733	1	US-07-640-029-4	Sequence 4, Appli
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489	129.5	8.4	822	2	US-07-807-133-1	Sequence 1, Appl
490	129.5	8.4	822	1	US-09-620-561-2	Sequence 2, Appl
491	129.5	8.4	822	2	US-08-451-822A-12	Sequence 12, Appl
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493	129.5	8.4	822	2	US-08-323-430-12	Sequence 12, Appl
494	129.5	8.4	822	2	US-09-620-561-2	Sequence 2, Appl
495	129.5	8.4	822	2	US-08-445-461-6	Sequence 6, Appl
496	129.5	8.4	354	2	US-10-104-047-2965	Sequence 2965, Ap
497	129	8.4	388	2	US-09-223-490-6	Sequence 6, Appli
498	129	8.4	388	1	US-09-667-135-2	Sequence 2, Appli
499	129	8.4	388	2	US-09-910-174B-29	Sequence 29, Appl
500	128	8.3	388	2	US-09-620-461-29	Sequence 29, Appl
501	128	8.3	388	2	US-09-270-767-44009	Sequence 44009, A
502	128.5	8.3	322	2	US-08-166-717D-6	Sequence 6, Appli
503	128.5	8.3	322	2	US-08-499-846-12	Sequence 12, Appl
504	128.5	8.3	322	2	US-08-447-314-6	Sequence 6, Appli
505	128.5	8.3	524	2	US-09-499-846-6	Sequence 6, Appli
506	128.5	8.3	820	1	US-08-499-846-10	Sequence 10, Appl
507	128.5	8.3	497	2	US-08-652-507-2	Sequence 2, Appli
508	128	8.3	497	2	US-09-383-586-33	Sequence 33, Appl
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511	127.5	8.3	322	2	US-08-475-458-2	Sequence 2, Appli
512	127.5	8.3	322	2	US-08-477-329-2	Sequence 2, Appli
513	127.5	8.3	322	2	US-08-168-195-2	Sequence 2, Appli
514	127.5	8.3	347	2	US-08-461-917-4	Sequence 4, Appli
515	127.5	8.3	424	6	5169835-6	Patent No. 5169835
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520	127.5	8.3	1106	1	US-08-168-195-2	Sequence 2, Appli
521	127.5	8.3	1106	1	US-08-477-329-2	Sequence 2, Appli
522	127.5	8.3	1106	1	US-08-475-458-2	Sequence 2, Appli
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524	127.5	8.3	1106	1	US-08-460-400-2	Sequence 2, Appli
525	127.5	8.3	1106	1	US-08-980-400-2	Sequence 2, Appli
526	127.5	8.3	1106	2	US-08-462-728-4	Sequence 4, Appli
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528	127.5	8.3	1106	2	US-09-583-210-2	Sequence 2, Appli
529	127.5	8.3	1106	2	US-09-583-449A-2	Sequence 2, Appli
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535	127.5	8.3	1106	2	US-09-866-510-18	Sequence 18, Appl
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554	126	8.2	767	1	US-08-874-678-2	Sequence 2, Appli
555	126	8.2	767	1	US-08-643-839-2	Sequence 2, Appli
556	126	8.2	767	2	US-08-886-2	Sequence 2, Appli
557	126	8.2	767	2	US-10-105-901A-2	Sequence 2, Appli
558	126	8.2	1356	1	US-08-810-116-8	Sequence 8, Appli
559	126	8.2	1356	1	US-07-930-548A-8	Sequence 8, Appli
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562	126	8.2	1356	2	US-09-949-016-6198	Sequence 6198, A
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564	126	8.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap
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570	125.5	8.1	398	2	US-08-441-893A-2	Sequence 2, Appli
571	125.5	8.1	471	2	US-09-949-016-9048	Sequence 9048, Ap
572	125.5	8.1	398	2	US-09-921-667-8	Sequence 8, Appli
573	125.5	8.1	398	4	PCT-US91-03478-2	Sequence 2, Appli
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577	125.5	8.1	471	2	US-09-949-016-9044	Sequence 9044, Ap
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587	125.5	8.1	596	2	US-09-991-326-13	Sequence 13, Appl
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593	125.5	8.1	612	2	US-09-991-326-11	Sequence 11, Appl
594	125.5	8.1	821	1	US-08-451-822A-13	Sequence 13, Appl
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596	125.5	8.1	1268	2	US-08-506-296B-28	Sequence 28, Appl
597	125	8.1	553	2	US-09-661-052-16	Sequence 16, Appl
598	125	8.1	553	1	US-09-188-082-16	Sequence 16, Appl
599	125	8.1	553	2	US-09-364-088-16	Sequence 16, Appl
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605	124.5	8.1	320	2	US-09-837-867A-2	Sequence 2, Appli
606	124.5	8.1	320	4	PCT-US95-02576-2	Sequence 2, Appli
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626	124	8.0	769	2	US-08-471-570-8	Sequence 8, Appli
627	123.5	8.0	262	2	US-10-104-047-3119	Sequence 3119, Ap
628	123.5	8.0	503	2	US-08-999-683A-6	Sequence 6, Appli
629	123.5	8.0	503	2	US-09-944-807-4	Sequence 4, Appli
630	123.5	8.0	885	2	US-10-104-162-2946	Sequence 2946, Ap
631	123.5	8.0	915	2	US-10-282-162-52	Sequence 52, Appl
632	123.5	8.0	917	2	US-10-282-162-54	Sequence 54, Appl
633	123.5	8.0	917	2	US-10-282-162-56	Sequence 56, Appl
634	123	8.0	299	2	US-10-282-200-15	Sequence 15, Appl
635	122.5	7.9	646	2	US-09-651-200-6728	Sequence 6728, Ap
636	122.5	7.9	646	2	US-09-949-016-6728	Sequence 6728, Ap
637	122.5	7.9	646	2	US-09-653-961-4	Sequence 4, Appli
638	122.5	7.9	826	2	US-09-877-730-16	Sequence 16, Appl
639	122.5	7.9	904	2	US-09-877-730-6	Sequence 6, Appli
640	122.5	7.9	907	2	US-09-877-730-20	Sequence 20, Appl
641	122.5	7.9	915	2	US-10-282-162-48	Sequence 48, Appl
642	122.5	7.9	917	2	US-10-282-162-50	Sequence 50, Appl
643	122.5	7.9	917	2	US-10-282-162-12	Sequence 12, Appl
644	122.5	7.9	985	2	US-09-877-730-12	Sequence 12, Appl
645	122.5	7.9	991	2	US-09-877-730-10	Sequence 10, Appl
646	122.5	7.9	1069	2	US-09-877-730-18	Sequence 18, Appl
647	122.5	7.9	1072	2	US-09-877-730-2	Sequence 2, Appli
648	122.5	7.9	771	2	US-08-247-247-4	Sequence 4, Appli
649	121.5	7.9	1209	2	US-09-130-158A-2	Sequence 2, Appli
650	121.5	7.9	216	2	US-09-130-299A-9	Sequence 9, Appli
651	122	7.9	351	4	PCT-US99-05703-2	Sequence 2, Appli
652	122	7.9	256	2	US-09-667-135-28	Sequence 28, Appl
653	122	7.9	373	2	US-09-823-038A-60	Sequence 60, Appl
654	122	7.9	525	4	PCT-US93-05703-2	Sequence 4, Appli
655	122	7.9	525	2	US-09-499-846-4	Sequence 4, Appli
656	122	7.9	622	2	US-09-499-846-8	Sequence 8, Appli
657	122	7.9	668	2	US-09-499-846-2	Sequence 2, Appli
658	122	7.9	771	2	US-09-173-151A-35	Sequence 35, Appl
659	121.5	7.9	404	2	US-09-799-152-1	Sequence 1, Appli
660	121.5	7.9	404	2	US-09-949-016-11025	Sequence 11025, A
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662	120.5	7.8	771	2	US-09-312-157-8	Sequence 8, Appli
663	121	7.8	771	2	US-08-279-707A-8	Sequence 8, Appli
664	121	7.8	771	2	US-09-717-888-8	Sequence 8, Appli
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667	120	7.8	404	2	US-09-638-649-3	Sequence 3, Appli
668	120.5	7.8	404	2	US-09-877-730-14	Sequence 14, Appl
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670	119.5	7.7	332	2	US-09-877-730-8	Sequence 8, Appli
671	119.5	7.7	380	2	US-09-046-736-2	Sequence 2, Appli
672	119.5	7.7	467	2	US-09-949-016-8293	Sequence 8293, Ap
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674	119	7.7	651	2	US-09-798-689-21	Sequence 21, Appl
675	118.5	7.7	238	2	US-08-902-486-11	Sequence 11, Appl
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677	118.5	7.7	239	2	US-08-999-689A-7	Sequence 7, Appli
678	118.5	7.7	512	2	US-08-999-689A-11	Sequence 11, Appl
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680	118.5	7.6	985	2	US-09-837-867A-211	Sequence 211, App
681	118	7.6	489	2	US-09-667-135-30	Sequence 30, Appl
682	118	7.6	489	2	US-10-020-445A-211	Sequence 211, App
683	118	7.6	795	2	US-09-949-016-7119	Sequence 7119, Ap
684	118	7.6	924	1	US-08-656-984A-28	Sequence 28, Appl

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685	118	7.6	924	1	US-08-485-604-28	Sequence 28, Appl
686	118	7.6	924	1	US-08-487-595-28	Sequence 28, Appli
687	117.5	7.6	328	2	US-09-560-639-9	Sequence 9, Appli
688	117.5	7.6	328	2	US-09-173-151A-25	Sequence 25, Appl
689	117.5	7.6	328	2	US-09-032-337-45	Sequence 45, Appl
690	117.5	7.6	328	2	US-09-949-016-6424	Sequence 6424, Ap
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692	117.5	7.6	403	2	US-09-638-649-5	Sequence 5, Appli
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695	117.5	7.6	544	2	US-09-999-833A-259	Sequence 259, App
696	117.5	7.6	544	2	US-10-020-445A-259	Sequence 259, App
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736	116.5	7.5	216	2	US-09-412-554A-2	Sequence 2, Appli
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738	116	7.5	732	2	US-09-291-299A-10	Sequence 10, Appl
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887	108.5	7.0	394	2	US-09-997-333-422	Sequence 422, App
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895	108	7.0	248	2	US-09-716-028-22	Sequence 22, Appl
896	108	7.0	248	2	US-10-113-996-22	Sequence 22, Appl
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958	106	7.0	252	1	US-08-398-613A-30	Sequence 30, Appl
959	106	7.0	278	2	US-09-355-014-27	Sequence 27, Appl
960	106	7.0	278	2	US-09-260-527-3	Sequence 3, Appli
961	106	7.0	286	2	US-09-270-767-44618	Sequence 44618, A
962	106	7.0	298	2	US-09-864-675-4	Sequence 4, Appli
963	106	7.0	330	2	US-09-864-675-2	Sequence 2, Appli
964	106	7.0	421	2	US-09-569-61C-36	Sequence 36, Appl
965	106	7.0	466	2	US-09-944-807-12	Sequence 12, Appl
966	106	7.0	466	2	US-09-949-016-6766	Sequence 6766, App
967	106	7.0	480	2	US-09-949-016-7272	Sequence 7272, App
968	106	7.0	483	2	US-09-310-463-16	Sequence 16, Appl
969	106	7.0	483	2	US-08-842-248A-16	Sequence 16, Appl
970	106	7.0	525	2	US-09-269-939A-6	Sequence 6, Appli
971	106	6.9	561	2	US-09-173-151A-23	Sequence 23, Appl
972	106	6.9	561	2	US-09-227-717-4	Sequence 67, Appl
973	106	6.9	561	2	US-09-775-046-15	Sequence 15, Appl
974	106	6.9	698	2	US-09-579-692B-60	Sequence 60, Appl
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981	106	6.9	1298	4	PCT-US95-04228-33	Sequence 33, Appl
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983	106	6.9	1362	2	US-08-643-839-33	Sequence 33, Appl
984	106	6.9	1362	2	US-09-348-886-33	Sequence 33, Appl
985	106	6.9	1362	2	US-10-105-901A-33	Sequence 33, Appl
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988	106	6.9	1363	2	US-08-643-839-32	Sequence 32, Appl
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996	106	6.9	1368	2	US-09-348-886-34	Sequence 34, Appl
997	106	6.9	1368	2	US-10-105-901A-34	Sequence 34, Appl
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1006	105.5	6.8	357	2	US-09-949-016-9074	Sequence 9074, Ap
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1013	105.5	6.8	442	1	US-08-462-571-5	Sequence 5, Appli
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1015	105.5	6.8	442	2	US-08-472-888A-7	Sequence 7, Appli
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1019	105.5	6.8	469	1	US-08-157-101A-7	Sequence 7, Appli
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1047	104.5	6.8	309	2	US-09-667-135-33	Sequence 33, Appl
1048	104.5	6.8	309	2	US-09-425-762-23	Sequence 23, Appl
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1064	104.5	6.8	340	2	US-09-188-930-184	Sequence 184, App
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1096	104	6.7	253	2	US-08-985-950-14	Sequence 14, Appl
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1119	103.5	6.7	615	2		Sequence 16, Appl
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1122	103	6.7	282	2		Sequence 66, Appl

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1127	103	6.7	451	2	US-09-466-635-3	Sequence 3, Appli
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1168	101.5	6.6	478	2	US-08-526-098-8	Sequence 8, Appli
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1171	101.5	6.6	410	2	US-09-698-705-13	Sequence 13, Appl
1172	101.5	6.6	486	2	US-09-432-016-6	Sequence 6, Appli
1173	101.5	6.6	486	1	US-08-684-594-6	Sequence 6, Appli
1174	101.5	6.6	738	6	526455-2	Patent No. 526454
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1178	101	6.5	253	2	US-09-027-449-52	Sequence 52, Appl
1179	101	6.5	253	2	US-08-804-444A-52	Sequence 52, Appl
1180	101	6.5	253	2	US-09-026-985-52	Sequence 52, Appl
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1202	101	6.5	900	2	US-10-282-162-40	Sequence 40, Appl
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1206	101	6.5	1518	2	US-09-487-558B-152	Sequence 152, Ap
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1216	100.5	6.5	229	2	US-09-716-028-26	Sequence 26, Appl
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1221	100.5	6.5	229	2	US-09-296-005-26	Sequence 26, Appl
1222	100.5	6.5	332	2	US-09-646-561-26	Sequence 26, Appl
1223	100.5	6.5	329	2	US-09-303-040-6	Sequence 6, Appli
1224	100.5	6.5	233	2	US-08-887-352B-26	Sequence 26, Appl
1225	100.5	6.5	268	2	US-09-651-200-18	Sequence 18, Appl
1226	100.5	6.5	233	2	US-09-282-846-2	Sequence 2, Appli
1227	100.5	6.5	329	2	US-09-282-846-2	Sequence 2, Appli
1228	100.5	6.5	233	1	US-09-680-145-2	Sequence 2, Appli
1229	100.5	6.5	233	2	US-08-887-352B-18	Sequence 18, Appl
1230	100.5	6.5	451	2	US-09-109-207C-18	Sequence 18, Appl
1231	100.5	6.5	451	2	US-09-920-171-18	Sequence 18, Appl
1232	100.5	6.5	451	2	US-09-716-028-18	Sequence 18, Appl
1233	100.5	6.5	451	2	US-09-282-505-2	Sequence 2, Appli
1234	100.5	6.4	451	2	US-09-296-005-18	Sequence 18, Appl
1235	100.5	6.4	451	1	US-08-459-657-43	Sequence 43, Appl
1236	100.5	6.4	451	2	US-09-282-846-2	Sequence 2, Appli
1237	100.5	6.4	451	2	US-08-887-352B-18	Sequence 18, Appl
1238	100.5	6.4	451	2	US-10-274-978-27	Sequence 27, Appl
1239	99.5	6.4	174	2	US-09-697-263-27	Sequence 27, Appl
1240	100	6.4	174	2	US-10-104-047-2303	Sequence 2303, Ap
1241	100	6.4	910	2	US-09-313-942-28	Sequence 28, Appl
1242	100	6.4	910	2	US-09-858-664A-26	Sequence 26, Appl
1243	99.5	6.4	174	1	US-10-282-162-43	Sequence 43, Appl
1244	99.5	6.4	174	4	US-08-466-465-8	Sequence 8, Appli
1245	99.5	6.4	259	2	US-09-719-243-2	Sequence 2, Appli
1246	99.5	6.4	259	2	US-10-104-047-2303	Sequence 2303, Ap
1247	99.5	6.4	339	2	US-07-940-861-43	Sequence 43, Appl
1248	99.5	6.4	347	2	US-09-443-588-2	Sequence 2, Appli
1249	99.5	6.4	347	1	US-08-459-512-43	Sequence 43, Appl
1250	99.5	6.4	347	1	US-08-887-352B-20	Sequence 20, Appl
1251	99.5	6.4	347	2	US-09-296-005-20	Sequence 20, Appl
1252	99.5	6.4	347	2	US-08-466-465-8	Sequence 8, Appli
1253	99.5	6.4	347	2	US-09-730-465-8	Sequence 8, Appli
1254	99.5	6.4	409	4	PCT-US92-02050-43	Sequence 43, Appl
1255	99.5	6.4	452	2	US-09-075-215A-17	Sequence 17, Appl
1256	99.5	6.4	409	2	US-09-773-877B-16	Sequence 16, Appl
1257	99	6.4	347	1	US-08-887-352B-20	Sequence 20, Appl
1258	99	6.4	229	2	US-09-109-207C-20	Sequence 20, Appl
1259	99	6.4	229	2	US-09-296-005-20	Sequence 20, Appl
1260	99	6.4	229	2	US-09-716-028-20	Sequence 20, Appl
1261	99	6.4	229	2	US-10-113-996-20	Sequence 20, Appl
1262	99	6.4	229	1	US-10-113-996-20	Sequence 20, Appl
1263	99	6.4	229	2	US-09-296-005-25	Sequence 25, Appl
1264	99	6.4	452	2	US-08-887-353B-25	Sequence 25, Appl
1265	99	6.4	233	2	US-09-109-207C-25	Sequence 25, Appl
1266	99	6.4	233	2	US-09-296-005-25	Sequence 25, Appl
1267	99	6.4	233	2	US-09-716-028-25	Sequence 25, Appl
1268	99	6.4	233	2	US-10-113-996-25	Sequence 25, Appl

1269	99	6.4	240	1	US-08-956-047-25	Sequence 25, Appl
1270	99	6.4	451	1	US-08-887-352B-14	Sequence 14, Appl
1271	99	6.4	451	2	US-08-887-352B-16	Sequence 16, Appl
1272	99	6.4	451	2	US-08-466-151-65	Sequence 65, Appl
1273	99	6.4	451	2	US-09-109-207C-14	Sequence 14, Appl
1274	99	6.4	451	2	US-09-109-207C-16	Sequence 16, Appl
1275	99	6.4	451	2	US-09-296-005-14	Sequence 14, Appl
1276	99	6.4	451	2	US-09-296-005-16	Sequence 16, Appl
1277	99	6.4	451	2	US-09-920-171-14	Sequence 14, Appl
1278	99	6.4	451	2	US-09-920-171-16	Sequence 16, Appl
1279	99	6.4	451	2	US-09-716-028-14	Sequence 14, Appl
1280	99	6.4	451	2	US-09-716-028-16	Sequence 16, Appl
1281	99	6.4	451	2	US-08-463-667A-14	Sequence 14, Appl
1282	99	6.4	451	2	US-08-564-164A-4	Sequence 4, Appl
1283	99	6.4	451	2	US-09-171-945-16	Sequence 16, Appli
1284	99	6.4	264	2	US-09-171-945-93	Sequence 93, Appl
1285	99	6.4	461	1	US-08-463-587A-26	Sequence 26, Appl
1286	99	6.4	461	2	US-08-923-854-26	Sequence 26, Appl
1287	99	6.4	461	4	US-09-197-945-95	Sequence 95, Appli
1288	99	6.4	461	2	PCT-US91-09133-27	Sequence 27, Appli
1289	99	6.4	825	1	US-08-162-809-16	Sequence 2, Appli
1290	99	6.4	983	2	US-09-949-016-11628	Sequence 11628, A
1291	98.5	6.4	238	1	US-09-949-486-57	Sequence 57, Appl
1292	98.5	6.4	246	1	US-09-469-658-57	Sequence 57, Appl
1293	98.5	6.4	260	2	US-09-171-945-93	Sequence 93, Appl
1294	98.5	6.4	260	2	US-09-171-945-93	Sequence 93, Appl
1295	98.5	6.4	264	2	US-08-564-164A-4	Sequence 4, Appl
1296	98.5	6.4	306	2	US-09-197-945-95	Sequence 95, Appl
1297	98.5	6.4	306	2	US-09-910-059-95	Sequence 95, Appl
1298	98.5	6.4	334	2	US-09-197-970B-7	Sequence 7, Appl
1299	98.5	6.4	440	2	US-09-866-028-61	Sequence 61, Appl
1300	98.5	6.4	440	2	US-09-944-457-61	Sequence 61, Appl
1301	98.5	6.4	440	2	US-09-944-457-61	Sequence 61, Appl
1302	98.5	6.4	440	2	US-09-945-584-61	Sequence 61, Appl
1303	98.5	6.4	440	2	US-09-944-944-61	Sequence 61, Appl
1304	98.5	6.4	442	2	US-09-778-510-20	Sequence 20, Appl
1305	98.5	6.4	442	2	US-09-930-803-1	Sequence 1, Appl
1306	98.5	6.4	478	2	US-10-104-3812	Sequence 3812, Ap
1307	98.5	6.4	613	2	US-09-171-945-113	Sequence 113, App
1308	98.5	6.4	613	2	US-09-910-059-113	Sequence 113, App
1309	98.5	6.4	716	2	US-09-171-945-125	Sequence 125, Appl
1310	98.5	6.4	716	2	US-09-910-059-125	Sequence 125, App
1311	98.5	6.4	832	2	US-08-630-820-7	Sequence 7, Appl
1312	98.5	6.4	832	2	US-09-273-453-7	Sequence 7, Appli
1313	98.5	6.4	239	1	US-08-353-400-37	Sequence 37, Appl
1314	98	6.3	309	2	US-09-079-029-9	Sequence 9, Appl
1315	98	6.3	451	2	US-09-925-179-68	Sequence 68, Appl
1316	98	6.3	460	2	US-10-630-406-5	Sequence 5, Appl
1317	98	6.3	513	2	US-09-174B-18	Sequence 18, Appl
1318	98	6.3	513	2	US-09-620-461-18	Sequence 18, Appl
1319	98	6.3	968	2	US-09-751-389-6	Sequence 6, Appl
1320	98	6.3	1123	2	US-09-949-016-6230	Sequence 6230, Ap
1321	98	6.3	1128	2	US-09-949-016-7522	Sequence 7522, Ap
1322	98	6.3	238	1	US-08-353-400-37	Sequence 37, Appl
1323	97.5	6.3	266	2	US-09-698-705-10	Sequence 10, Appl
1324	97.5	6.3	293	6	US-09-746-311B-114	Sequence 114, App
1325	97.5	6.3	353	2	5189147-3	Patent No. 5189147
1326	97.5	6.3	330	1	US-09-203-958A-4	Sequence 4, Appli
1327	97.5	6.3	330	1	US-09-040-774-2	Sequence 2, Appli
1328	97	6.3	1241	2	US-08-332-562A-81	Sequence 81, Appl
1329	97	6.3	365	2	US-08-332-562A-134	Sequence 134, App
1330	97	6.3	482	2	US-08-875-811-53	Sequence 53, Appl
1331	97	6.3	541	2	US-09-509-031-16	Sequence 16, Appl
1332	97	6.3	541	2	US-10-071-485-85	Sequence 85, Appl
1333	97	6.3	581	2	US-10-071-485-85	Sequence 85, Appl
1334	97	6.3	581	2	US-08-724-394A-2	Sequence 2, Appl
1335	97	6.3	789	2	US-09-831-846-2	Sequence 2, Appl
1336	96.5	6.3	222	1	US-08-458-516-22	Sequence 22, Appl
1337	96.5	6.2	235	2	US-08-458-516-23	Sequence 23, Appl
1338	96.5	6.2	240	1	US-09-485-737B-91	Sequence 91, Appl
1339	96.5	6.2	240	2	US-09-485-737B-91	Sequence 91, Appl
1340	96.5	6.2	244	2	US-10-071-485-91	Sequence 91, Appli
1341	96.5	6.2	244	2	US-09-244-369B-1	Sequence 1, Appli
1342	96.5	6.2	245	1	US-08-918-148-78	Sequence 78, Appl
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1344	96.5	6.2	263	2	US-09-293-533-66	Sequence 66, Appl
1345	96.5	6.2	278	2	US-09-570-367C-21	Sequence 21, Appl
1346	96.5	6.2	278	2	US-09-915-524-21	Sequence 21, Appl
1347	96.5	6.2	278	2	US-09-934-634-21	Sequence 21, Appl
1348	96.5	6.2	283	2	US-09-917-278-21	Sequence 21, Appl
1349	96.5	6.2	288	2	US-08-332-562A-136	Sequence 136, App
1350	96.5	6.2	288	1	US-08-147-772-2	Sequence 2, Appl
1351	96.5	6.2	288	1	US-08-456-104-6	Sequence 6, Appl
1352	96.5	6.2	288	2	US-08-101-624-23	Sequence 23, Appl
1353	96.5	6.2	288	1	US-08-751-767A-6	Sequence 6, Appl
1354	96.5	6.2	288	2	US-08-153-262-2	Sequence 2, Appl
1355	96.5	6.2	288	2	US-08-702-525-19	Sequence 19, Appl
1356	96.5	6.2	288	2	US-09-205-697A-19	Sequence 19, Appl
1357	96.5	6.2	288	2	US-09-159-135-2	Sequence 2, Appl
1358	96.5	6.2	288	2	US-08-479-744A-29	Sequence 29, Appl
1359	96.5	6.2	288	2	US-08-450-798-2	Sequence 2, Appl
1360	96.5	6.2	288	2	US-08-453-386A-2	Sequence 2, Appli
1361	96.5	6.2	288	2	US-08-403-253A-2	Sequence 2, Appl
1362	96.5	6.2	288	2	US-09-206-132-6	Sequence 29, Appli
1363	96.5	6.2	288	2	US-09-425-516-29	Sequence 29, Appli
1364	96.5	6.2	288	2	US-09-350-202-2	Sequence 2, Appl
1365	96.5	6.2	288	2	US-09-651-200-13	Sequence 13, Appl
1366	96.5	6.2	288	2	US-09-667-135-34	Sequence 34, Appl
1367	96.5	6.2	288	2	US-08-435-816A-2	Sequence 2, Appl
1368	96.5	6.2	288	2	US-09-425-762-29	Sequence 29, Appl
1369	96.5	6.2	288	2	US-08-667-867A-19	Sequence 19, Appl
1370	96.5	6.2	288	2	US-09-837-667A-19	Sequence 19, Appl
1371	96.5	6.2	288	2	US-09-910-174B-5	Sequence 5, Appl
1372	96.5	6.2	288	2	US-09-620-461-5	Sequence 5, Appli
1373	96.5	6.2	288	2	US-09-915-789A-15	Sequence 15, Appl
1374	96.5	6.2	288	2	US-09-349-915B-2	Sequence 2, Appl
1375	96.5	6.2	288	2	US-08-592-711-2	Sequence 2, Appli
1376	96.5	6.2	288	4	PCT-US95-02576-19	Sequence 19, Appl
1377	96.5	6.2	449	1	US-08-458-516-13	Sequence 13, Appl
1378	96	6.2	969	2	US-09-949-016-8059	Sequence 8059, Ap
1379	96	6.2	2864	1	US-09-469-260A-394	Sequence 394, App
1380	96	6.2	2864	2	US-08-488-446-394	Sequence 394, App
1381	96.5	6.2	2864	2	US-08-467-344A-394	Sequence 394, App
1382	96	6.2	2864	2	US-08-424-550B-394	Sequence 394, App
1383	96	6.2	139	1	US-08-182-067-10	Sequence 10, Appl
1384	96	6.2	139	2	US-08-465-313-10	Sequence 10, Appl
1385	96	6.2	139	2	US-09-809-739-5	Sequence 5, Appl
1386	96	6.2	139	2	US-09-378-967-10	Sequence 10, Appl
1387	96	6.2	155	1	US-09-378-967-6	Sequence 6, Appl
1388	96	6.2	155	2	US-08-494-577-6	Sequence 6, Appli
1389	96	6.2	155	1	US-08-494-577-7	Sequence 7, Appli
1390	96	6.2	155	2	US-08-795-868-6	Sequence 6, Appl
1391	96	6.2	155	2	US-08-795-868-7	Sequence 7, Appl
1392	96	6.2	155	2	US-09-303-069-6	Sequence 6, Appli
1393	96	6.2	155	2	US-09-303-069-7	Sequence 7, Appli
1394	96	6.2	222	2	US-09-134-250-6	Sequence 6, Appl
1395	96	6.2	250	2	US-09-134-250-7	Sequence 7, Appl
1396	96	6.2	261	2	US-09-893-737-108	Sequence 108, App
1397	96	6.2	261	2	US-10-194-975-110	Sequence 110, App
1398	96	6.2	266	6	US-09-270-767-32698	Sequence 32698, A
1399	96	6.2	495	2	US-09-270-767-48115	Sequence 48115, A
1400	96	6.2	582	6	5175384-11	Patent No. 5175384
1401	96	6.2	582	2	US-09-948-004-18	Sequence 18, Appl
1402	96	6.2	582	2	US-09-702-705-334	Sequence 334, App
1403	96	6.2	582	2	US-09-736-457-334	Sequence 334, App
1404	96	6.2	582	2	US-09-614-124B-334	Sequence 334, App
1405	96	6.2	582	2	US-09-671-325-334	Sequence 334, App
1406	96	6.2	582	2	US-09-589-184-334	Sequence 334, App
1407	96	6.2	582	2	US-09-658-824-334	Sequence 334, App
1408	96	6.2	582	2	US-10-017-754-334	Sequence 334, App
1409	96	6.2	582	2	US-09-651-553-334	Sequence 334, App
1410	96	6.2	583	1	US-09-519-642-334	Sequence 334, App
1411	96	6.2	583	2	US-08-432-016-2	Sequence 2, Appl
1412	96	6.2	583	2	US-08-684-594-2	Sequence 2, Appl
1413	95.5	6.2	604	2	US-08-949-016-9548	Sequence 9548, Ap
1414	95.5	6.2	232	2	US-08-425-763-2	Sequence 2, Appli
1415	—	—	232	1	US-08-811-757-2	Sequence 2, Appl

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1415	95.5	6.2	232	2	US-09-249-210-2	Sequence 2, Appli
1416	95.5	6.2	235	2	US-09-649-672A-12	Sequence 12, Appl
1417	95.5	6.2	242	1	US-08-398-613A-56	Sequence 56, Appl
1418	95.5	6.2	242	1	US-08-398-612A-56	Sequence 56, Appl
1419	95.5	6.2	242	1	US-08-398-611A-56	Sequence 56, Appl
1420	95.5	6.2	242	2	US-08-491-334A-56	Sequence 56, Appl
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1423	95.5	6.2	242	2	US-09-026-985-42	Sequence 42, Appl
1424	95.5	6.2	242	2	US-09-121-952A-42	Sequence 42, Appl
1425	95.5	6.2	242	2	US-09-234-340A-42	Sequence 42, Appl
1426	95.5	6.2	242	2	US-09-355-014-42	Sequence 42, Appl
1427	95.5	6.2	257	2	US-08-411-295F-78	Sequence 78, Appl
1428	95.5	6.2	258	1	US-08-860-174A-13	Sequence 13, Appl
1429	95.5	6.2	310	2	US-09-079-029-11	Sequence 11, Appl
1430	95.5	6.2	423	2	US-09-778-510-22	Sequence 22, Appl
1431	95.5	6.2	462	2	US-09-773-877B-18	Sequence 18, Appl
1432	95.5	6.2	474	2	US-09-848-832-3	Sequence 3, Appli
1433	95.5	6.2	504	2	US-09-270-767-43244	Sequence 43244, A
1434	95.5	6.2	581	2	US-09-499-522-18	Sequence 18, Appl
1435	95.5	6.2	581	2	US-09-269-939A-12	Sequence 12, Appl
1436	95.5	6.2	782	2	US-09-456-090A-98	Sequence 98, Appl
1437	95.5	6.2	875	2	US-09-453-234-98	Sequence 98, Appl
1438	95.5	6.2	945	2	US-08-702-525-65	Sequence 65, Appl
1439	95.5	6.2	92	6	Patent No. 5284931-8	Patent No. 5284931
1440	95.5	6.2	139	1	US-08-039-198B-10	Sequence 10, Appl
1441	95.5	6.2	212	1	US-08-702-525-63	Sequence 63, Appl
1442	95.5	6.2	212	4	PCT-US95-02576-63	Sequence 63, Appl
1443	95.5	6.2	225	2	US-09-456-090A-98	Sequence 98, Appl
1444	95.5	6.2	225	2	US-09-453-234-98	Sequence 98, Appl
1445	95.5	6.2	226	2	US-08-702-525-65	Sequence 65, Appl
1446	95.5	6.2	226	2	US-09-915-789A-21	Sequence 21, Appl
1447	95.5	6.2	226	4	PCT-US95-02576-65	Sequence 65, Appl
1448	95.5	6.2	235	2	US-09-485-737B-93	Sequence 93, Appl
1449	95.5	6.2	235	2	US-10-071-485-93	Sequence 93, Appl
1450	95.5	6.2	255	2	US-09-171-945-19	Sequence 19, Appl
1451	95.5	6.2	255	2	US-09-910-059-19	Sequence 19, Appl
1452	95.5	6.2	421	1	US-08-759-628-5	Sequence 5, Appli
1453	95.5	6.2	454	1	US-07-934-373C-22	Sequence 22, Appl
1454	95.5	6.2	454	2	US-08-437-642B-22	Sequence 22, Appl
1455	95.5	6.2	454	2	US-08-146-206C-22	Sequence 22, Appl
1456	95.5	6.2	454	2	US-09-705-686-22	Sequence 22, Appl
1457	95.5	6.2	454	2	US-09-705-392A-22	Sequence 22, Appl
1458	95.5	6.2	454	4	PCT-US93-07832-22	Sequence 22, Appl
1459	95.5	6.2	454	2	US-09-705-398-22	Sequence 22, Appl
1460	95.5	6.2	467	2	US-08-523-894-8	Sequence 8, Appli
1461	95.5	6.2	467	2	US-08-523-894-10	Sequence 10, Appl
1462	95.5	6.2	473	2	US-09-171-945-131	Sequence 131, App
1463	95.5	6.2	473	2	US-09-910-059-131	Sequence 131, App
1464	95.5	6.2	475	2	US-09-740-002-27	Sequence 27, Appl
1465	95.5	6.2	777	2	US-08-874-678-3	Sequence 3, Appli
1466	95.5	6.2	777	2	US-08-643-839-3	Sequence 3, Appli
1467	95.5	6.2	777	2	US-09-348-886-3	Sequence 3, Appli
1468	95.5	6.2	777	1	US-10-105-901A-3	Sequence 3, Appli
1469	95.5	6.2	902	2	US-10-282-162-36	Sequence 36, Appl
1470	95.5	6.2	2316	2	US-09-949-002-314	Sequence 314, App
1471	95	6.2	2415	2	US-09-949-002-398	Sequence 398, App
1472	94.5	6.2	95	2	US-09-928-383B-17	Sequence 17, Appl
1473	94.5	6.2	223	2	US-08-190-199A-63	Sequence 63, Appl
1474	94.5	6.2	237	2	US-09-746-311B-22	Sequence 22, Appl
1475	94.5	6.2	240	1	US-08-488-111B-148	Sequence 148, App
1476	94.5	6.2	240	1	US-08-477-484B-148	Sequence 148, App
1477	94.5	6.2	240	2	US-08-646-360-148	Sequence 148, App
1478	94.5	6.2	240	2	US-08-839-765-148	Sequence 148, App
1479	94.5	6.2	240	2	US-09-136-389-148	Sequence 148, App
1480	94.5	6.2	240	2	US-09-610-838-148	Sequence 148, App
1481	94.5	6.2	240	2	US-09-711-485-148	Sequence 148, App
1482	94.5	6.2	245	2	US-09-138-091A-76	Sequence 76, Appl
1483	94.5	6.2	253	2	US-08-833-488B-20	Sequence 20, Appl
1484	94.5	6.2	254	1	US-08-792-824-4	Sequence 4, Appli
1485	94.5	6.1	254	1	US-08-792-824-7	Sequence 7, Appli
1486	94.5	6.1	254	1	US-08-792-824-10	Sequence 10, Appl
1487	94.5	6.1	254	1	US-08-792-824-13	Sequence 13, Appl
1488	94.5	6.1	270	2	US-09-976-118-2	Sequence 2, Appli
1489	94.5	6.1	313	2	US-09-756-983-15	Sequence 15, Appl
1490	94.5	6.1	360	2	US-09-949-016-8370	Sequence 8370, Ap
1491	94.5	6.1	432	2	US-08-477-460B-2	Sequence 2, Appli
1492	94.5	6.1	432	2	US-09-379-516-2	Sequence 2, Appli
1493	94.5	6.1	432	2	US-09-322-916-2	Sequence 2, Appli
1494	94.5	6.1	432	2	US-09-485-372A-2	Sequence 2, Appli
1495	94.5	6.1	432	2	US-09-409-006A-2	Sequence 2, Appli
1496	94.5	6.1	432	2	US-08-484-681-2	Sequence 2, Appli
1497	94.5	6.1	432	2	US-09-766-999-2	Sequence 2, Appli
1498	94.5	6.1	432	4	PCT-US93-07422-2	Sequence 2, Appli
1499	94.5	6.1	467	1	US-08-704-744-81	Sequence 81, Appl
1500	94.5	6.1	557	2	US-09-773-877B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-188-930-331
Sequence 331, Application US/09188930A
Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011C1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGGNSYG 120

Qy  121  EVXVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  EVXVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy  241  AAVLVTLILLLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AAVLVTLILLLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
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RESULT 2
US-09-462-270-2
Sequence 2, Application US/09462270
Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface

```
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-7015OUS
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match          100.0%;  Score 1544;  DB 2;  Length 299;
Best Local Similarity 100.0%;  Pred. No. 8.3e-135;
Matches 299;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60

Qy   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120

Qy  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180

Qy  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240

Qy  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299


RESULT 3
US-09-254-465A-1
; Sequence 1, Application US/0925465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match          100.0%;  Score 1544;  DB 2;  Length 299;
Best Local Similarity 100.0%;  Pred. No. 8.3e-135;
Matches 299;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60

Qy   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120

Qy  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180

Qy  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240

Qy  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299


RESULT 4
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-189

Query Match          100.0%;  Score 1544;  DB 2;  Length 299;
Best Local Similarity 100.0%;  Pred. No. 8.3e-135;
Matches 299;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  60

Qy   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG  120

Qy  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST  180

Qy  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  240

Qy  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV  299
```

RESULT 5
US-09-312-283C-331
Sequence 331, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onnst, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-331

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYYTCMVSEBGGNSYG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYYTCMVSEBGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFPDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFPDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 6
US-09-907-794A-119
Sequence 119, Application US/0907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Pisvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US/09/907,794A
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-119

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYYTCMVSEBGGNSYG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYYTCMVSEBGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFPDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299

Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 7
US-09-905-125A-119
; Sequence 119, Application US/0905125A
; Patent No. 6664376
; GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-119

Query Match   100.0%;   Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%;   Pred. No. 8.3e-135;
Matches 299; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGTKAQVERKLLCLFILAILLLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 8
US-09-902-775A-119
; Sequence 119, Application US/0902775A
; Patent No. 6686451
; GENERAL INFORMATION:
APPLICANT: Genentech, Inc
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-119

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy 121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPSEYTWFKDGIVMPTNPKST 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPSEYTWFKDGIVMPTNPKST 180

Qy 181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy 241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 9
US-09-397-243D-3
; Sequence 3, Application US/09397243D
; Patent No. 6699688
; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-243D-3

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFPDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy 121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPSEYTWFKDGIVMPTNPKST 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSPSEYTWFKDGIVMPTNPKST 180

Qy 181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy 241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 10
US-09-906-700-119
; Sequence 119, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-119

Query Match   100.0%;   Score 1544;   DB 2;   Length 299;
Best Local Similarity   100.0%;   Pred. No. 8.3e-135;
Matches 299; Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGNSYG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGNSYG 120

Qy   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGVGTPMTSNAVRMEAVERNVGVIV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGVGTPMTSNAVRMEAVERNVGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.161B2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-119

Query Match   100.0%;   Score 1544;   DB 2;   Length 299;
Best Local Similarity   100.0%;   Pred. No. 8.3e-135;
Matches 299; Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEGGNSYG 120

RESULT 11
US-09-903-603A-119
; Sequence 119, Application US/0903603A
; Patent No. 6767995
; GENERAL INFORMATION:

RESULT 12
US-09-904-920A-119
; Sequence 119, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/904,920A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match   100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity   100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSSEPEVRIPENNPVKLSCAYSGFSSPRV 60

Qy   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYG 120

Qy   121 EVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 EVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV 299

RESULT 13
US-09-909-064-119
; Sequence 119, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

. RESULT 14

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; ORGANISM: Homo sapiens
; TYPE: PRT
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; NUMBER OF SEQ ID NOS: 423
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
CURRENT FILING DATE: 2001-07-18
CURRENT APPLICATION NUMBER: US/09/909,064
FILE REFERENCE: 10466-14
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
APPLICANT: Wood, William. I.

Query Match 100.0%; Score 1544; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.3e-135;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-905-381A-119
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; TYPE: PRT
; LENGTH: 299
SEQ ID NO 119
; NUMBER OF SEQ ID NOS: 423
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30911
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PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 2000-01-05
CURRENT FILING DATE: 2001-07-13
CURRENT APPLICATION NUMBER: US/09/905,381A
FILE REFERENCE: 10466-14
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
APPLICANT: Wood, William. I.
APPLICANT: Williams, P. Mickey
APPLICANT: Tumas, Daniel
APPLICANT: Stewart, Timothy A.
APPLICANT: Roy, Margaret Ann
APPLICANT: Pacni, Nicholas F.
APPLICANT: Pan, James
APPLICANT: Mather, Jennie P.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Gurney, Austin L.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Godowski, Paul J.
APPLICANT: Goddard, A.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerber, Hanspeter
APPLICANT: Gao, Wei-Qiang
APPLICANT: Fong, Sherman
APPLICANT: Filvaroff, Ellen
APPLICANT: Ferrara, Napoleone
APPLICANT: Eaton, Dan L.
APPLICANT: Desnoyers, Luc
APPLICANT: Botstein, David
APPLICANT: Ashkenazi, Avi
APPLICANT: Genentech, Inc.
GENERAL INFORMATION:
Patent No. 6818746
Sequence 119, Application US/09905381A

US-09-905-381A-119

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Best Local Similarity   100.0%;   Score 1544; DB 2; Length 299;
Matches 299; Conservative   0;   Pred. No. 8.3e-135; Mismatches   0; Indels   0; Gaps   0;

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RESULT 15
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Patent No. 6828146
GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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PRIOR APPLICATION NUMBER: US 60/145,698
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US-09-906-618-119

Query Match
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Matches 299; Conservative   0;   Pred. No. 8.3e-135; Mismatches   0; Indels   0; Gaps   0;

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                              SUMMARIES

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627	428	27.7	298	5	US-10-481-090A-2	Sequence 2, Appli
628	427	27.7	310	3	US-10-481-090A-3	Sequence 3, Appli
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701	424	27.5	310	3	US-09-833-245-2046	Sequence 2046, Ap
702	424	27.5	310	3	US-09-833-245-2047	Sequence 2047, Ap
709	424	27.5	310	3	US-09-833-244-20	Sequence 20, Appl
727	424	27.5	310	4	US-10-050-704-163	Sequence 163, Appl
728	424	27.5	310	4	US-10-050-704-164	Sequence 164, Appl
729	424	27.5	310	4	US-10-050-704-109	Sequence 109, App1
855	424	27.5	310	4	US-10-223-085-262	Sequence 262, App
858	424	27.5	310	4	US-10-223-084-262	Sequence 262, App
859	424	27.5	310	4	US-10-223-088-262	Sequence 262, App
860	424	27.5	310	4	US-10-223-090-262	Sequence 262, App
861	424	27.5	310	4	US-10-223-087-262	Sequence 262, App
863	424	27.5	310	4	US-10-223-083-262	Sequence 262, App
864	424	27.5	310	4	US-10-223-089-262	Sequence 262, App
993	424	27.5	310	4	US-10-265-542-31	Sequence 31, Appl
1007	424	27.5	310	4	US-10-299-976-423	Sequence 423, App
1022	424	27.5	310	4	US-10-299-937-423	Sequence 423, App
1025	424	27.5	310	4	US-10-223-081-262	Sequence 262, App
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1152	424	27.5	310	4	US-10-266-829-65	Sequence 65, Appl
1153	424	27.5	310	4	US-10-266-829-90	Sequence 90, Appl
1154	424	27.5	310	4	US-10-266-829-91	Sequence 91, Appl
1155	424	27.5	310	4	US-10-305-654-262	Sequence 262, App
1156	424	27.5	310	4	US-10-448-923-423	Sequence 423, App
1157	424	27.5	310	4	US-10-439-249-20	Sequence 20, Appl
1158	424	27.5	310	4	US-10-449-656-423	Sequence 423, App
1159	424	27.5	310	4	US-10-448-713-423	Sequence 423, App
1162	424	27.5	310	4	US-10-425-447-423	Sequence 423, App
1169	424	27.5	310	4	US-10-081-056-262	Sequence 262, App
1173	424	27.5	310	4	US-10-601-953-888	Sequence 888, App
1174	424	27.5	310	4	US-10-633-008-31	Sequence 31, Appl
1176	424	27.5	310	4	US-10-215-371-423	Sequence 423, App
1177	424	27.5	310	4	US-10-797-366-423	Sequence 423, App
1178	424	27.5	310	4	US-10-798-512-109	Sequence 109, App
1179	424	27.5	310	4	US-10-798-512-163	Sequence 163, App
1180	424	27.5	310	4	US-10-798-512-164	Sequence 164, App
1181	424	27.5	310	4	US-10-692-072-20	Sequence 20, Appl
1182	424	27.5	310	4	US-10-771-187-423	Sequence 423, App
1192	424	27.5	310	4	US-10-931-886-538	Sequence 538, App
1194	424	27.5	310	4	US-10-963-467-423	Sequence 423, App
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1196	424	27.5	310	5	US-10-955-952-538	Sequence 538, App
1197	424	27.5	310	5	US-10-878-523-65	Sequence 65, Appl
1198	424	27.5	310	5	US-10-878-523-90	Sequence 90, Appl
1199	424	27.5	310	4	US-10-970-823-423	Sequence 423, App
1200	424	27.5	310	4	US-10-878-523-91	Sequence 91, Appl
1201	424	27.5	329	4	US-10-264-049-3034	Sequence 3034, Ap
1202	424	27.5	339	4	US-10-266-829-113	Sequence 113, App
1203	424	27.5	339	5	US-10-878-523-113	Sequence 113, App
1204	412	26.7	76	5	US-10-785-351-9	Sequence 9, Appli
1205	409	26.5	76	5	US-10-785-351-11	Sequence 11, Appl
1208	404	26.2	312	3	US-09-905-291A-64	Sequence 64, Appl
1209	404	26.2	312	3	US-09-953-499-9	Sequence 9, Appli

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Run on: May 16, 2006, 07:12:26 ; Search time 115 Seconds
                  (without alignments)
                  122.067 Million cell updates/sec

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GenCore version 5.1.8

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Perfect score: 1544
Sequence: 1 MGTKAQVERKLLCLFILAIL........YSQPSARSEGEFKQTSSFLV 299

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 250354

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
2	1544	100.0	299	9	US-10-973-115B-366	Sequence 366, App
3	1544	100.0	299	11	US-11-000-463-275	Sequence 275, App
4	1544	100.0	299	11	US-11-000-463-747	Sequence 747, App
5	1544	100.0	299	11	US-10-536-366-1	Sequence 538, Appli
6	1544	100.0	299	11	US-11-000-463-748	Sequence 748, App
7	1544	100.0	299	11	US-11-173-037-7	Sequence 7, Appli
8	1544	100.0	299	11	US-11-290-153-366	Sequence 366, App
9	1544	100.0	299	11	US-11-290-153-1300	Sequence 1300, Ap
10	1544	100.0	299	11	US-11-264-096-1300	Sequence 1300, Ap
11	1544	100.0	299	11	US-11-264-096-1301	Sequence 1301, Ap
12	1281	83.0	259	11	US-11-000-463-276	Sequence 276, App
13	1281	67.9	300	11	US-11-025-834A-276	Sequence 21, Appl
14	431	27.9	298	9	US-10-536-366-1	Sequence 1, Appl
	1048.5	27.9	298		US-10-973-115B-538	Sequence 538, Appl
16	424	27.5	310	9	US-10-536-366-1	Sequence 15, Appl
20	424	27.5	310	11	US-11-025-834A-15	Sequence 538, App
21	424	27.5	310	11	US-11-290-153-538	Sequence 2045, App
22	424	27.5	310	11	US-11-264-096-2045	Sequence 2045, App
23	424	27.5	310	11	US-11-264-096-2046	Sequence 2047, App
24	424	27.5	310	11	US-11-264-096-2047	Sequence 2047, Ap
25	424	27.5	362	9	US-10-821-224-1148	Sequence 1148, App
26	419	27.1	310	9	US-10-536-366-3	Sequence 3, Appl
27	415	26.9	310	11	US-11-025-834A-13	Sequence 13, Appl
29	404	26.2	312	9	US-11-973-115B-336	Sequence 336, App
32	404	26.2	312	11	US-11-290-153-336	Sequence 336, App
33	404	26.2	323	9	US-11-536-366-4	Sequence 336, App
34	391	25.3	298	11	US-11-025-834A-14	Sequence 14, Appli
35	390	25.3	212	11	US-11-025-834A-16	Sequence 16, Appl
36	326.5	21.1	265	11	US-11-025-834A-16	Sequence 42, Appl
37	282	18.3	265	9	US-10-453-372-3709	Sequence 3709, Ap
43	229	13.9	229	9	US-10-453-372-1090	Sequence 1090, App
44	214.5	13.9	1902	9	US-10-453-372-1084	Sequence 1084, App
45	213.5	13.8	5636	8	US-10-453-372-1086	Sequence 1086, Ap
51	213.5	13.8	365	11	US-10-453-372-1088	Sequence 1088, Ap
52	207.5	13.4	365	11	US-11-264-096-2152	Sequence 2152, Ap
53	207.5	13.4	373	9	US-11-159-919-2	Sequence 2, Appli
55	207.5	13.4	373	11	US-11-159-919-4	Sequence 4, Appli
64	196	12.7	396	11	US-11-264-096-1236	Sequence 1236, Ap
65	189	12.2	399	11	US-11-264-096-1237	Sequence 1237, Ap
66	182	11.8	961	11	US-11-501-841-61	Sequence 61, Appl
67	182	11.8	1068	9	US-10-995-561-860	Sequence 860, App
68	181	11.8	1068	9	US-10-995-561-861	Sequence 861, App
69	181	11.7	1077	9	US-10-995-561-863	Sequence 863, App
70	181	11.7	1093	9	US-10-995-561-864	Sequence 864, App
77	179.5	11.6	316	11	US-10-995-561-865	Sequence 865, App
79	178.5	11.6	321	11	US-11-264-096-680	Sequence 680, App
80	178.5	11.6	399	11	US-10-453-372-682	Sequence 682, App
81	178.5	11.6	399	11	US-10-453-372-686	Sequence 686, App
82	178	11.6	399	11	US-10-453-372-688	Sequence 688, App
83	177.5	11.5	847	9	US-10-453-372-690	Sequence 690, App
84	177.5	11.5	488	9	US-10-453-372-694	Sequence 694, App
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86	177.5	11.5	847	9	US-10-453-372-35	Sequence 35, Appl
87	177	11.5	847	9	US-10-501-561-865	Sequence 865, App
89	176	11.4	390	11	US-10-973-115B-338	Sequence 338, App
92	176	11.4	390	11	US-11-290-153-338	Sequence 338, App
93	176	11.4	707	9	US-10-453-372-728	Sequence 728, App
94	176	11.4	712	9	US-10-453-372-712	Sequence 712, App
95	174.5	11.3	782	9	US-10-453-372-714	Sequence 714, App
97	174.5	11.3	398	9	US-10-453-372-1000	Sequence 1000, App
100	174	11.3	1709	11	US-10-973-115B-348	Sequence 348, App
101	173	11.2	1709	9	US-10-453-372-666	Sequence 666, App
102	173	11.2	1709	9	US-10-453-372-732	Sequence 732, App
103	173	11.2	1709	11	US-11-135-855-35	Sequence 35, Appl
104	173	11.2	457	9	US-10-453-372-410	Sequence 410, App
105	172	11.1	457	9	US-10-453-372-690	Sequence 690, App
106	172	11.1	460	9	US-10-453-372-688	Sequence 688, App
107	473	11.1	473	9	US-10-453-372-686	Sequence 686, App
108	473	11.1	473	9	US-10-453-372-694	Sequence 694, App
109	473	11.1	473	9	US-10-453-372-698	Sequence 698, App
110	650	11.1	650	11	US-11-072-512-3395	Sequence 3395, Ap
111	652	11.1	652	9	US-10-453-372-722	Sequence 722, App
112	172	11.1	172	9	US-10-453-372-724	Sequence 724, App
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123	172	11.1	2617	9	US-10-453-372-732	Sequence 732, App
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134	670	11.1	670	9	US-10-973-115B-352	Sequence 352, App
137	1119	11.1	1119	9	US-10-821-224-1148	Sequence 1148, App
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139	396	10.9	396	9	US-10-493-909-79	Sequence 79, Appl

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143	168	10.9	317	11	US-11-072-512-3036	Sequence 3036, Ap
144	167.5	10.9	473	11	US-10-453-372-696	Sequence 696, Appl
145	167.5	10.8	1571	11	US-11-134-587B-12	Sequence 12, Appl
146	167.5	10.8	1700	9	US-10-453-372-416	Sequence 416, App
147	167.5	10.8	1910	11	US-11-134-587B-2	Sequence 2, Appli
148	167.5	10.8	1910	11	US-11-134-587B-3	Sequence 3, Appli
149	165	10.8	344	11	US-11-080-991-4	Sequence 4, Appli
150	165	10.7	344	11	US-11-186-284-20	Sequence 20, Appli
151	165	10.7	344	11	US-11-077-386-16	Sequence 16, Appli
152	165	10.7	344	11	US-11-077-224B-4	Sequence 4, Appli
153	165	10.7	344	11	US-11-050-857-56	Sequence 56, Appli
154	165	10.7	344	11	US-11-097-252A-4	Sequence 4, Appli
155	165	10.7	344	11	US-11-050-857-959	Sequence 959, App
156	164.5	10.7	1694	11	US-11-135-855-36	Sequence 36, Appl
157	164.5	10.6	473	11	US-10-453-372-684	Sequence 684, App
158	162.5	10.5	1700	9	US-10-453-372-398	Sequence 398, App
159	162.5	10.5	548	9	US-10-453-372-754	Sequence 754, App
160	162.5	10.5	548	9	US-10-453-372-768	Sequence 768, App
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161	162.5	10.5	1700	9	US-10-453-372-414	Sequence 414, App
162	162.5	10.5	1700	9	US-10-453-372-418	Sequence 418, App
161.5		10.5	1571	11	US-11-134-587B-13	Sequence 13, Appl
162.5		10.5	543	9	US-10-453-372-756	Sequence 756, App
163	160.6	10.6	473	11	US-10-453-372-684	Sequence 684, App
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165	160.5	10.5	548	9	US-10-453-372-754	Sequence 754, App
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167	160.5	10.4	766	9	US-10-453-372-752	Sequence 752, App
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170	157.5	10.4	977	11	US-11-093-274-29	Sequence 39, Appl
172	157.5	10.2	734	11	US-11-093-274-40	Sequence 40, Appl
181	157	10.2	344	11	US-10-973-115B-376	Sequence 376, Appl
182	156.5	10.1	555	9	US-10-453-372-764	Sequence 764, App
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185	153	9.9	1338	11	US-10-505-928-857	Sequence 857, App
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187	153	9.9	1338	11	US-11-075-047A-2	Sequence 2, Appl
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194	152.5	9.8	324	11	US-11-077-386-15	Sequence 15, Appl
195	151.5	9.8	582	11	US-11-051-724-94	Sequence 94, Appl
196	151	9.8	4419	11	US-10-821-234-1155	Sequence 1155, Ap
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203	150	9.7	569	8	US-11-050-857-552	Sequence 552, App
204	150	9.7	702	11	US-11-538-066-363	Sequence 363, App
205	150	9.7	702	11	US-11-033-039-282	Sequence 282, App
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210	150	9.7	719	11	US-11-051-720-1381	Sequence 1381, Ap
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215	149	9.7	450	9	US-11-290-153-378	Sequence 378, App
216	149	9.7	526	8	US-11-505-928-160	Sequence 160, Appl
217	149	9.7	647	11	US-11-080-991-32	Sequence 32, Appl
218	149	9.7	739	11	US-11-493-909-69	Sequence 69, Appl
219	149	9.7	739	11	US-11-107-028-6	Sequence 6, Appli
220	149	9.7	3588	9	US-10-995-561-672	Sequence 672, App
221	149	9.7	4346	11	US-10-995-561-671	Sequence 671, App
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224	148.5	9.6	1315	9	US-10-453-372-1034	Sequence 1034, Ap
225	148.5	9.6	1335	9	US-10-453-372-1030	Sequence 1030, Ap
226	146	9.5	394	8	US-10-538-066-754	Sequence 754, App
227	146	9.5	702	9	US-11-510-101-68	Sequence 68, Appl
228	145	9.4	758	11	US-11-043-693-1	Sequence 1, Appli
229	145	9.4	1912	11	US-11-288-493-64	Sequence 64, Appl

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232	144	9.3	319	9	US-10-453-372-300	Sequence 300, App
233	144	9.3	765	11	US-11-172-410-19	Sequence 19, Appl
234	144	9.3	490	11	US-11-051-720-325	Sequence 325, App
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237	143.5	9.3	504	11	US-11-051-720-1699	Sequence 1699, Ap
238	143.5	9.3	504	11	US-11-051-720-1700	Sequence 1700, Ap
239	143.5	9.3	504	9	US-10-453-372-308	Sequence 308, App
240	143.5	9.3	504	11	US-11-186-284-20	Sequence 20, App
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242	143.5	9.3	584	11	US-11-051-720-324	Sequence 324, App
243	143.5	9.3	315	9	US-10-453-372-316	Sequence 316, App
244	143	9.3	325	9	US-10-453-372-290	Sequence 290, App
245	143	9.3	344	9	US-11-051-720-368	Sequence 368, App
246	142.5	9.2	289	11	US-11-299-182-12	Sequence 12, Appl
247	142	9.2	325	9	US-10-311-822-11	Sequence 11, Appl
248	142	9.2	325	9	US-10-453-372-306	Sequence 306, App
249	141	9.2	319	9	US-10-453-372-292	Sequence 292, App
250	141.5	10	531	10	US-10-453-372-296	Sequence 296, App
251	141.5	9.2	626	11	US-10-453-372-312	Sequence 312, App
252	141	9.1	1493	11	US-11-180-855-1	Sequence 1, Appli
253	141	9.1	307	9	US-10-453-372-298	Sequence 298, App
254	141	9.1	309	9	US-10-453-372-294	Sequence 294, App
255	141	9.1	319	9	US-10-453-372-312	Sequence 312, App
256	141	9.1	320	9	US-10-453-372-310	Sequence 310, App
257	141	9.1	325	9	US-10-453-372-294	Sequence 294, App
258	141	9.1	336	9	US-10-453-372-308	Sequence 308, App
259	141	9.1	336	9	US-10-453-372-310	Sequence 310, App
260	141	9.1	336	9	US-10-453-372-314	Sequence 314, App
261	141	9.1	336	9	US-10-453-372-316	Sequence 316, App
262	141	9.1	717	11	US-11-050-857-954	Sequence 954, App
263	141	9.1	717	11	US-11-051-720-1695	Sequence 1695, Ap
264	141	9.1	860	11	US-11-172-410-2	Sequence 2, Appli
265	141	9.1	1461	11	US-11-183-136-28	Sequence 28, Appl
266	140.5	9.1	345	9	US-11-093-274-758	Sequence 758, App
267	140.5	9.1	429	11	US-11-093-274-337	Sequence 37, Appl
268	140	9.1	309	9	US-10-453-372-302	Sequence 302, App
269	140	9.1	336	9	US-10-453-372-282	Sequence 282, App
270	140	9.1	336	9	US-10-453-372-318	Sequence 318, App
271	138.5	9.0	1745	11	US-11-264-096-2222	Sequence 2222, Ap
272	138	8.9	517	11	US-11-051-720-1432	Sequence 1432, Ap
273	137.5	8.9	335	9	US-10-948-716-5	Sequence 5, Appli
274	137	8.9	1189	11	US-11-050-857-953	Sequence 953, App
275	137	8.9	1189	11	US-11-051-720-1694	Sequence 1694, Ap
276	136.5	8.8	357	9	US-10-453-372-760	Sequence 760, App
277	136.5	8.8	1180	8	US-10-505-928-459	Sequence 459, App
278	136.5	8.8	1192	9	US-10-745-586-130	Sequence 130, App
279	136.5	8.8	1299	11	US-11-169-041-231	Sequence 231, App
280	136	8.8	555	9	US-10-821-234-1015	Sequence 1015, Ap
281	136	8.8	236	11	US-11-137-465-61	Sequence 61, Appl
282	135.5	8.7	442	9	US-10-821-234-B2	Sequence 394, App
283	134	8.7	253	9	US-10-453-372-288	Sequence 288, App
284	134	8.7	628	11	US-11-080-991-108	Sequence 108, App
285	133.5	8.6	398	11	US-10-996-628-4	Sequence 4, Appli
286	133.5	8.6	398	11	US-11-223-492-6	Sequence 6, Appli
287	133.5	8.6	426	9	US-10-948-716-1	Sequence 1, Appli
288	133.5	8.6	428	9	US-10-948-716-3	Sequence 3, Appli
289	133.5	8.6	696	9	US-10-948-716-758	Sequence 758, App
290	133.5	8.6	740	11	US-10-453-372-368	Sequence 368, App
291	133	8.6	1250	9	US-11-137-465-62	Sequence 62, Appl
292	133	8.6	477	11	US-10-973-115B-50	Sequence 50, Appl
293	133	8.6	477	11	US-11-290-153-50	Sequence 50, Appl
294	132.5	8.6	1193	11	US-11-139-435-3	Sequence 3, Appli
295	132	8.6	342	11	US-11-094-519A-39	Sequence 39, Appl
296	132	8.5	1193	11	US-11-329-258-23	Sequence 23, Appl
302	131.5	8.5	1007	9	US-11-094-519A-39	Sequence 39, Appl
303	131.5	8.5	1191	11	US-11-183-567A-2	Sequence 2, Appl
305	132	8.5	822	9	US-11-139-435-2	Sequence 2, Appli
306	132	8.5	424	9	US-11-183-567A-2	Sequence 2, Appl
307	131.5	8.5	822	11	US-10-948-716-6	Sequence 6, Appli
313	130.5	8.5	696	9	US-10-453-372-336	Sequence 336, App
314	130.5	8.5	696	9	US-10-453-372-320	Sequence 320, App
315	130.5	8.5	757	9	US-10-453-372-350	Sequence 350, App
316	130.5	8.5	757	9	US-10-453-372-350	Sequence 350, App

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320	130	8.4	529	11	US-11-186-541-1	Sequence 1, Appli
321	129.5	8.4	417	8	US-10-505-928-664	Sequence 664, App
322	129.5	8.4	1343	11	US-10-541-814-15	Sequence 15, Appl
323	129	8.4	354	11	US-11-072-512-2965	Sequence 2965, A
338	128.5	8.4	419	9	US-10-948-716-4	Sequence 4, Appli
339	128.5	8.3	696	9	US-10-453-372-324	Sequence 324, App
340	128.5	8.3	696	9	US-10-453-372-346	Sequence 346, App
341	128.5	8.3	696	9	US-10-453-372-354	Sequence 354, App
342	128.5	8.3	696	9	US-10-453-372-356	Sequence 356, App
343	128.5	8.3	696	9	US-10-453-372-358	Sequence 358, App
344	128.5	8.3	700	9	US-10-453-372-326	Sequence 326, App
345	128.5	8.3	1343	11	US-10-541-814-2	Sequence 2, Appl
346	128	8.3	696	9	US-10-453-372-362	Sequence 362, App
347	127.5	8.3	246	11	US-11-266-444-1630	Sequence 1630, A
348	127.5	8.3	696	9	US-10-453-372-364	Sequence 364, App
349	127.5	8.3	696	11	US-11-266-444-1630	Sequence 1630, A
350	127.5	8.3	1106	11	US-11-075-047A-16	Sequence 16, Appl
351	127.5	8.3	1106	11	US-11-076-427A-16	Sequence 16, Appl
352	127.5	8.3	1106	11	US-11-075-047A-119	Sequence 119, App
353	127	8.2	248	11	US-11-054-515-1963	Sequence 1963, A
354	127	8.2	248	11	US-11-266-444-1963	Sequence 1963, A
355	127	8.2	515	11	US-11-093-274-38	Sequence 38, Appl
356	126.5	8.2	250	11	US-11-054-515-1529	Sequence 1529, A
357	126.5	8.2	250	11	US-11-266-444-1529	Sequence 1529, A
358	126.5	8.2	1433	11	US-11-094-519A-40	Sequence 40, Appl
360	126	8.2	708	9	US-10-511-538-229	Sequence 229, App
365	126	8.2	764	9	US-10-995-561-905	Sequence 905, App
366	126	8.2	764	9	US-10-995-561-904	Sequence 904, App
367	126	8.2	764	11	US-11-104-111-28	Sequence 28, Appl
368	126	8.2	767	9	US-11-043-693-2	Sequence 2, Appli
369	126	8.2	1306	9	US-10-995-561-905	Sequence 905, App
370	126	8.2	1356	9	US-10-995-561-904	Sequence 904, App
371	126	8.2	1356	9	US-10-995-561-906	Sequence 906, App
372	125.5	8.1	398	8	US-10-511-937-2405	Sequence 2405, A
373	125.5	8.1	398	9	US-10-821-234-1583	Sequence 1583, A
374	125.5	8.1	419	9	US-10-821-234-1664	Sequence 1664, A
375	125.5	8.1	419	11	US-11-104-111-28	Sequence 28, Appl
376	124.5	8.1	917	9	US-10-493-909-76	Sequence 76, Appl
377	124.5	8.1	917	9	US-10-948-716-7	Sequence 7, Appli
378	124	8.0	249	11	US-11-054-515-1272	Sequence 1272, A
379	124	8.0	249	11	US-11-266-444-1272	Sequence 1272, A
380	124	8.0	253	11	US-11-054-515-1199	Sequence 1199, A
381	124	8.0	253	11	US-11-266-444-1199	Sequence 1199, A
382	124	8.0	336	9	US-10-453-372-304	Sequence 304, App
383	124	8.0	686	11	US-11-051-724-52	Sequence 52, Appl
384	124	8.0	822	9	US-10-493-909-75	Sequence 254, App
385	123.5	8.0	248	11	US-11-054-515-1785	Sequence 1785, A
386	123.5	8.0	248	11	US-11-266-444-1785	Sequence 1785, A
387	123.5	8.0	262	11	US-11-072-512-3119	Sequence 3119, A
388	123.5	8.0	466	9	US-10-979-095-1	Sequence 1, Appli
389	123.5	8.0	696	9	US-10-453-372-360	Sequence 360, App
390	123.5	8.0	885	11	US-11-072-52-2946	Sequence 2946, A
391	123.5	8.0	915	11	US-11-144-987-22	Sequence 22, Appl
392	123.5	8.0	915	11	US-11-205-935-22	Sequence 22, Appl
393	123.5	8.0	917	11	US-11-144-987-24	Sequence 24, Appl
394	123.5	8.0	917	11	US-11-205-935-24	Sequence 24, Appl
395	123.5	8.0	917	11	US-11-144-987-26	Sequence 26, Appl
396	123.5	8.0	917	11	US-11-205-935-26	Sequence 26, Appl
397	123	8.0	248	11	US-11-054-515-2070	Sequence 2070, A
398	123.5	7.9	248	11	US-11-266-444-2070	Sequence 2070, A
399	122.5	7.9	335	9	US-10-948-716-10	Sequence 10, Appl
400	122.5	7.9	424	9	US-10-948-716-2	Sequence 2, Appl
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402	122.5	7.9	915	11	US-11-205-935-16	Sequence 16, Appl
403	122.5	7.9	917	11	US-11-144-987-18	Sequence 18, Appl
404	122.5	7.9	917	11	US-11-205-935-18	Sequence 18, Appl
405	122.5	7.9	917	11	US-11-144-987-20	Sequence 20, Appl
406	122.5	7.9	917	11	US-11-205-935-20	Sequence 20, Appl
407	122.5	7.9	249	11	US-11-139-435-1	Sequence 1, Appli
408	122	7.9	1150	11	US-11-054-515-1347	Sequence 1347, Ap
409	122	7.9	249	11	US-11-266-444-1347	Sequence 1347, Ap
410	122	7.9	338	11	US-11-124-367A-471	Sequence 471, App
411	122	7.9	842	11	US-11-124-368A-171	Sequence 171, App
412	121.5	7.9	244	11	US-11-054-515-1513	Sequence 1513, Ap
413	121.5	7.9	244	11	US-11-266-444-1513	Sequence 1513, Ap
414	121.5	7.9	255	9	US-10-514-534-8	Sequence 8, Appli
415	121.5	7.9	256	11	US-11-054-515-1253	Sequence 1253, Ap
416	121.5	7.9	256	11	US-11-266-444-1253	Sequence 1253, Ap
417	121.5	7.9	258	11	US-11-054-515-1255	Sequence 1255, Ap
418	121.5	7.9	258	11	US-11-266-444-1255	Sequence 1255, Ap
419	121.5	7.9	404	11	US-11-197-038-1	Sequence 1, Appli
420	121.5	7.9	404	11	US-11-197-038-2	Sequence 2, Appli
421	121.5	7.9	404	11	US-11-050-857-58	Sequence 58, Appl
422	121	7.9	404	11	US-11-186-422-2	Sequence 2, Appli
423	121	7.8	247	11	US-11-005-843-1	Sequence 1, Appli
424	121	7.8	247	11	US-11-054-515-1429	Sequence 1429, Ap
425	121	7.8	249	11	US-11-266-444-1429	Sequence 1429, Ap
426	121	7.8	249	11	US-11-054-515-1296	Sequence 1296, Ap
427	120.5	7.8	577	9	US-11-266-444-1296	Sequence 1296, Ap
428	120.5	7.8	242	11	US-10-493-909-66	Sequence 66, Appl
429	120.5	7.8	242	11	US-11-054-515-1580	Sequence 1580, Ap
430	120.5	7.8	256	11	US-11-266-444-1580	Sequence 1580, Ap
431	120.5	7.8	277	9	US-11-050-857-58	Sequence 58, Appl
432	120.5	7.8	712	11	US-11-264-096-1856	Sequence 1856, A
433	120.5	7.8	757	9	US-10-453-372-352	Sequence 352, App
434	120	7.8	773	9	US-10-453-372-348	Sequence 348, App
435	120.5	7.8	778	9	US-10-453-372-330	Sequence 330, App
436	120	7.7	23	9	US-11-173-037-1	Sequence 1, Appli
437	120	7.8	245	11	US-11-054-515-1757	Sequence 1757, A
438	120	7.8	245	11	US-11-266-444-1757	Sequence 1757, A
439	120	7.8	253	11	US-11-054-515-1298	Sequence 1298, A
440	120	7.8	253	11	US-11-266-444-1298	Sequence 1298, A
441	119.5	7.8	218	9	US-10-995-561-830	Sequence 830, App
442	119.5	7.7	246	11	US-11-054-515-1393	Sequence 1393, A
443	119.5	7.7	246	11	US-11-266-444-1393	Sequence 1393, A
444	119.5	7.7	270	9	US-11-266-798-23	Sequence 23, Appl
445	119.5	7.7	328	8	US-10-233-798-23	Sequence 23, Appl
446	119.5	7.7	467	11	US-10-505-928-597	Sequence 597, App
447	119	7.7	686	11	US-10-246-019A-2	Sequence 2, Appli
448	119	7.7	686	11	US-11-051-724-48	Sequence 48, Appl
449	119	7.7	192	9	US-11-051-724-46	Sequence 46, Appl
450	119	7.7	713	9	US-10-453-372-322	Sequence 322, App
451	118.5	7.7	192	9	US-10-514-534-9	Sequence 9, Appli
452	118.5	7.7	246	11	US-11-054-515-1996	Sequence 1996, A
453	118.5	7.7	246	11	US-11-266-444-1996	Sequence 1996, A
454	118.5	7.7	248	11	US-11-054-515-1040	Sequence 1040, A
455	118.5	7.7	248	11	US-11-266-444-1040	Sequence 1040, A
456	118.5	7.7	467	11	US-11-000-463-452	Sequence 452, App
457	118.5	7.7	467	11	US-11-000-463-924	Sequence 924, App
458	118.5	7.7	467	11	US-11-000-463-925	Sequence 925, App
459	118	7.7	912	9	US-10-493-909-75	Sequence 75, Appl
460	118	7.7	245	11	US-11-054-515-1477	Sequence 1477, A
462	118	7.7	245	11	US-11-266-444-1477	Sequence 1477, A
463	118	7.6	422	11	US-10-917-905-3	Sequence 3, Appli
464	118	7.6	245	10	US-11-251-465-22	Sequence 22, Appl
465	118	7.6	806	9	US-10-857-780-20	Sequence 20, Appl
466	118	7.6	924	9	US-10-493-909-67	Sequence 67, Appl
467	117.5	7.6	924	9	US-11-107-028-26	Sequence 26, Appl
468	118	7.6	924	11	US-11-266-444-1639	Sequence 1639, A
469	117.5	7.6	244	11	US-11-054-515-1639	Sequence 1639, A
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474	117.5	7.6	328	9	US-10-501-033-333	Sequence 333, App
475	117.5	7.6	374	11	US-10-246-019A-4	Sequence 4, Appli
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483	117.5	7.6	1084	9	US-10-517-905-23	Sequence 23, Appl
484	117.5	7.6	1085	9	US-10-517-905-6	Sequence 6, Appli
485	117.5	7.6	1086	9	US-10-517-905-8	Sequence 8, Appli
486	117.5	7.6	1089	9	US-10-517-905-2	Sequence 2, Appli
487	117.5	7.6	1089	9	US-10-517-905-4	Sequence 4, Appli
488	117.5	7.6	1089	9	US-10-517-905-21	Sequence 21, Appl

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492	117.5	7.6	1089	11	US-11-076-427A-14	Sequence 14, Appl
493	117.5	7.6	1089	11	US-11-075-047A-117	Sequence 117, Appl
494	117.5	7.6	1089	11	US-11-177-894-26	Sequence 26, Appl
495	117.5	7.6	1089	11	US-11-177-894-27	Sequence 27, Appl
496	117.5	7.6	1089	11	US-11-177-894-28	Sequence 28, Appl
497	117.5	7.6	1089	11	US-11-177-894-29	Sequence 29, Appl
498	117.5	7.6	1089	11	US-11-233-510-28	Sequence 28, Appl
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501	117	7.6	249	11	US-10-995-561-829	Sequence 829, Appl
502	117	7.6	257	11	US-10-995-515-1753	Sequence 1753, Ap
503	117	7.6	257	11	US-11-266-444-1240	Sequence 14, Appl
504	117	7.6	276	11	US-11-087-901-19	Sequence 1240, Ap
505	117	7.6	305	11	US-11-266-444-898	Sequence 19, Appl
506	117	7.6	305	11	US-11-266-444-898	Sequence 898, App
507	117	7.6	391	11	US-11-087-177-13	Sequence 11, Appli
508	117	7.6	250	11	US-10-996-628-2	Sequence 2, Appl
509	116.5	7.5	250	11	US-11-054-515-1203	Sequence 1203, Ap
510	116.5	7.5	250	11	US-11-054-515-1212	Sequence 1212, Ap
511	116.5	7.5	250	11	US-11-266-444-1203	Sequence 1203, Ap
512	116.5	7.5	250	11	US-11-266-444-1212	Sequence 1212, Ap
513	116.5	7.5	252	11	US-11-054-515-898	Sequence 898, App
514	116.5	7.5	252	11	US-11-266-444-898	Sequence 898, App
515	116.5	7.5	259	9	US-10-995-561-883	Sequence 883, App
516	116.5	7.5	349	11	US-11-235-776A-13	Sequence 13, Appl
517	116.5	7.5	426	9	US-10-948-716-9	Sequence 9, Appl
518	116.5	7.5	458	11	US-11-235-776A-11	Sequence 3, Appl
519	116.5	7.5	543	9	US-10-495-664-3	Sequence 51, Appl
520	116	7.5	602	9	US-10-493-909-51	Sequence 51, Appl
521	116	7.5	648	9	US-10-917-905-6	Sequence 6, Appli
522	116	7.5	263	11	US-11-054-515-1278	Sequence 1278, Ap
523	116	7.5	263	11	US-11-266-444-1278	Sequence 1278, Ap
524	116	7.5	305	11	US-11-266-444-1278	Sequence 13, Appl
525	116	7.5	341	9	US-10-080-091-13	Sequence 13, Appl
526	115.5	7.5	238	11	US-10-514-534-6	Sequence 6, Appli
527	115.5	7.5	238	11	US-11-052-554A-51	Sequence 51, Appl
528	115.5	7.5	240	11	US-11-052-554A-52	Sequence 52, Appl
529	115.5	7.5	248	11	US-11-000-463-248	Sequence 248, Appl
530	115.5	7.5	248	11	US-11-054-515-1387	Sequence 1387, Ap
531	115.5	7.5	250	11	US-11-266-444-1387	Sequence 1387, Ap
532	115.5	7.5	250	11	US-10-054-515-1370	Sequence 1370, Ap
533	115.5	7.5	277	9	US-11-266-444-1370	Sequence 1370, Ap
534	115.5	7.5	374	11	US-11-000-463-453	Sequence 453, App
535	115.5	7.5	381	11	US-11-197-644-3	Sequence 3, Appl
536	115.5	7.5	382	11	US-11-197-038-3	Sequence 1788, Ap
537	115.5	7.5	382	11	US-11-197-038-2	Sequence 2, Appli
538	115.5	7.5	426	11	US-11-197-644-2	Sequence 2, Appli
539	115.5	7.5	595	11	US-11-266-444-1585	Sequence 1585, Ap
540	115.5	7.5	290	9	US-10-821-224-2258	Sequence 2258, Ap
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542	115	7.4	283	9	US-11-266-444-1788	Sequence 1422, Ap
543	115	7.4	308	9	US-10-453-372-850	Sequence 850, App
544	115	7.4	290	9	US-10-453-372-836	Sequence 836, App
545	115	7.4	290	9	US-10-453-372-842	Sequence 842, App
546	115	7.4	290	9	US-10-453-372-848	Sequence 848, App
547	115	7.4	290	11	US-11-113-424-77	Sequence 4, Appli
548	115	7.4	290	11	US-11-245-713-1	Sequence 77, Appl
549	115	7.4	595	11	US-11-264-096-763	Sequence 1, Appli
550	115	7.4	295	9	US-10-453-372-840	Sequence 763, App
551	115	7.4	290	11	US-11-235-776A-1	Sequence 840, App
552	115	7.4	339	11	US-11-197-038-4	Sequence 1, Appli
553	115	7.4	339	11	US-11-005-843-2	Sequence 4, Appli
554	115	7.4	339	11	US-11-197-644-4	Sequence 2, Appli
555	115	7.4	346	11	US-11-197-038-35	Sequence 4, Appli
556	115	7.4	346	11	US-11-197-644-35	Sequence 35, Appl
557	115	7.4	548	11	US-11-197-038-35	Sequence 35, Appl
558	115	7.4	551	11	US-11-235-776A-3	Sequence 7, Appli
559	115	7.4	551	11	US-11-235-776A-7	Sequence 9, Appli
560	115	7.4	551	11	US-11-235-776A-9	Sequence 9, Appl
561	114.5	7.4	244	11	US-11-054-515-1210	Sequence 1210, Ap

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562	114.5	7.4	244	11	US-11-054-515-1214	Sequence 1214, Ap
563	114.5	7.4	244	11	US-11-266-444-1210	Sequence 1210, Ap
564	114.5	7.4	252	11	US-11-054-515-1129	Sequence 1129, Ap
565	114.5	7.4	252	11	US-11-266-444-1129	Sequence 1129, Ap
566	114.5	7.4	266	9	US-10-995-561-544	Sequence 544, App
567	114.5	7.4	269	9	US-10-839-799-109	Sequence 109, App
568	114.5	7.4	352	11	US-11-051-720-1325	Sequence 1325, Ap
569	114.5	7.4	354	11	US-11-051-720-1324	Sequence 1324, Ap
570	114.5	7.4	409	9	US-10-821-234-892	Sequence 892, Appl
571	114.5	7.4	409	11	US-11-198-819-8	Sequence 8, Appli
572	114.5	7.4	439	11	US-11-219-563-132	Sequence 132, App
573	114.5	7.4	439	10	US-11-219-563-132	Sequence 132, App
574	114.5	7.4	464	11	US-11-218-813-132	Sequence 132, App
575	114.5	7.4	464	11	US-11-218-813-132	Sequence 132, App
576	114	7.4	247	11	US-11-054-515-1455	Sequence 1455, Ap
577	114	7.4	247	11	US-11-266-444-1455	Sequence 1455, Ap
578	114	7.4	248	11	US-11-054-515-1976	Sequence 1976, Ap
579	114	7.4	248	11	US-11-266-444-1976	Sequence 1976, Ap
580	114	7.4	251	11	US-11-054-515-1536	Sequence 1536, Ap
581	114	7.4	251	11	US-11-266-444-1536	Sequence 1536, Ap
582	114	7.4	305	9	US-10-055-877-126	Sequence 126, App
583	114	7.4	305	9	US-10-055-877-264	Sequence 264, App
584	114	7.4	305	11	US-11-054-515-1546	Sequence 1546, Ap
585	114	7.4	305	11	US-11-266-444-1546	Sequence 1546, Ap
586	114	7.4	346	11	US-11-050-720-1383	Sequence 1383, Ap
587	114	7.4	346	11	US-11-051-720-1383	Sequence 1383, Ap
588	114	7.4	461	11	US-11-197-644-32	Sequence 32, Appl
589	114	7.4	461	11	US-11-197-038-32	Sequence 32, Appl
590	113.5	7.4	249	11	US-11-054-515-1188	Sequence 1188, Ap
591	113.5	7.4	249	11	US-11-266-444-1188	Sequence 1188, Ap
592	113.5	7.4	251	11	US-11-054-515-1546	Sequence 1546, Ap
593	113.5	7.3	251	11	US-11-266-444-1546	Sequence 1546, Ap
594	113.5	7.4	258	11	US-11-054-515-1243	Sequence 1243, Ap
595	113.5	7.4	258	11	US-11-266-444-1243	Sequence 1243, Ap
596	113.5	7.4	269	11	US-11-224-726-1	Sequence 1, Appli
597	113.5	7.4	288	9	US-10-821-234-1062	Sequence 1062, Ap
598	113.5	7.4	297	9	US-10-453-372-766	Sequence 766, App
599	113	7.3	22	11	US-11-173-037-2	Sequence 2, Appli
600	113	7.3	194	11	US-11-173-037-3	Sequence 3, Appli
601	113	7.3	447	9	US-10-884-730-379	Sequence 379, App
602	113	7.3	448	11	US-11-299-182-18	Sequence 18, Appl
603	113	7.3	489	11	US-11-299-182-14	Sequence 14, Appl
604	113	7.3	652	11	US-11-299-182-4	Sequence 4, Appli
605	112.5	7.3	248	11	US-11-197-038-32	Sequence 32, Appl
606	112.5	7.3	248	11	US-11-054-515-2086	Sequence 2086, Ap
607	112.5	7.3	250	11	US-11-266-444-2086	Sequence 2086, Ap
608	112.5	7.3	250	11	US-11-266-444-1348	Sequence 1348, Ap
609	112.5	7.3	421	11	US-11-051-724-98	Sequence 98, Appl
610	112.5	7.3	421	11	US-11-051-724-96	Sequence 96, Appl
611	112.5	7.3	463	11	US-11-102-240-86	Sequence 86, Appl
612	112.5	7.3	463	11	US-11-103-195-86	Sequence 86, Appl
613	112.5	7.3	463	11	US-11-072-512-2048	Sequence 2048, Ap
617	112.5	7.3	245	11	US-11-266-444-1430	Sequence 1430, Ap
618	112.5	7.3	245	11	US-11-266-444-1422	Sequence 1422, Ap
619	112.5	7.3	22	10	US-11-173-037-3	Sequence 3, Appli
620	112	7.3	245	11	US-11-266-444-1348	Sequence 1348, Ap
621	112	7.3	245	11	US-11-266-444-1464	Sequence 1464, Ap
622	112	7.3	245	11	US-11-054-515-1847	Sequence 1847, Ap
623	112	7.3	245	11	US-11-266-444-1847	Sequence 1847, Ap
624	112	7.3	245	11	US-11-054-515-1754	Sequence 1754, Ap
625	112	7.3	245	11	US-11-054-515-1464	Sequence 1464, Ap
626	112	7.3	245	11	US-11-054-515-1422	Sequence 1422, Ap
627	112	7.3	245	11	US-11-266-444-1430	Sequence 1430, Ap
628	112	7.3	245	11	US-11-266-444-1464	Sequence 1464, Ap
629	112	7.3	245	9	US-11-264-096-763	Sequence 1754, Ap
630	112	7.3	245	11	US-11-266-444-1794	Sequence 1794, Ap
631	112	7.3	246	11	US-11-054-515-1847	Sequence 1847, Ap
632	112	7.3	246	11	US-11-266-444-1847	Sequence 1847, Ap
633	112	7.3	247	11	US-11-266-444-878	Sequence 878, App
634	112	7.3	247	11	US-11-054-515-878	Sequence 878, App
635	112	7.3	248	11	US-11-266-444-2000	Sequence 2000, Ap
636	112	7.3	248	11	US-11-054-515-2000	Sequence 2000, Ap
637	112	7.3	259	11	US-11-266-444-1497	Sequence 1497, App
638	112	7.3	259	11	US-11-054-515-1497	Sequence 1497, App
639	112	7.3	267	9	US-11-720-561-543	Sequence 543, App
640	112	7.3	363	11	US-10-995-561-1326	Sequence 1326, Ap

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641	112	7.3	421	11	US-11-051-724-100	Sequence 100, Appl
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644	111.5	7.2	242	11	US-11-054-515-1438	Sequence 1438, Ap
645	111.5	7.2	242	11	US-11-054-515-1507	Sequence 1507, Ap
646	111.5	7.2	244	11	US-11-054-515-1842	Sequence 1842, Ap
647	111.5	7.2	244	11	US-11-054-515-2058	Sequence 2058, Ap
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673	111	7.2	255	11	US-11-054-515-863	Sequence 863, App
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675	111	7.2	257	11	US-11-054-515-1553	Sequence 1553, Ap
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677	111	7.2	327	11	US-11-233-798-2	Sequence 2, Appl
678	111	7.2	336	11	US-11-113-424-83	Sequence 83, Appl
679	110.5	7.2	244	11	US-11-054-515-1491	Sequence 1491, Ap
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686	110.5	7.2	248	11	US-11-266-444-1273	Sequence 1273, Ap
687	110.5	7.2	248	11	US-11-266-444-1331	Sequence 1331, Ap
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694	110.5	7.2	254	11	US-11-054-515-1600	Sequence 1600, Ap
695	110.5	7.2	256	11	US-11-266-444-1600	Sequence 1600, Ap
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707	110	7.1	302	9	US-10-453-372-782	Sequence 782, App
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709	110	7.1	473	9	US-11-453-372-770	Sequence 770, App
710	109.5	7.1	248	11	US-11-054-515-1254	Sequence 1254, Ap
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727	109.5	7.1	738	9	US-10-995-561-693	Sequence 693, App
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734	109	7.1	240	11	US-11-054-515-1905	Sequence 1905, Ap
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736	109	7.1	248	9	US-11-266-444-1528	Sequence 1528, Ap
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751	109	7.1	316	11	US-11-197-038-6	Sequence 6, Appl
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755	109	7.1	323	11	US-11-197-644-6	Sequence 6, Appl
756	109	7.1	324	11	US-11-197-038-37	Sequence 37, Appl
757	109	7.1	324	11	US-11-197-038-36	Sequence 36, Appl
758	109	7.1	324	11	US-11-054-515-1275	Sequence 1275, Ap
759	109	7.1	402	11	US-11-197-644-36	Sequence 36, Appl
760	109	7.1	412	9	US-11-174-150-47	Sequence 47, Appl
761	109	7.1	516	11	US-11-185-436-20	Sequence 20, Appl
762	109	7.1	516	11	US-11-186-422-6	Sequence 6, Appl
763	109	7.1	526	11	US-11-236-198-19	Sequence 19, Appl
764	109	7.1	628	9	US-10-453-372-548	Sequence 548, App
765	109	7.1	628	9	US-10-917-905-1	Sequence 1, Appli
766	109	7.1	640	9	US-10-917-905-4	Sequence 4, Appli
767	109	7.1	640	9	US-10-973-115B-368	Sequence 368, App
768	109	7.1	640	9	US-10-917-905-1	Sequence 1, Appli
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772	109	7.1	402	11	US-11-174-150-47	Sequence 47, Appl
773	109	7.1	324	11	US-11-197-038-36	Sequence 36, Appl
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775	109	7.1	324	11	US-11-197-038-37	Sequence 37, Appl
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777	109	7.1	316	9	US-10-453-372-550	Sequence 550, App
778	109	7.1	628	9	US-10-453-372-550	Sequence 550, App
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782	109	7.1	516	9	US-11-054-515-1367	Sequence 1367, Ap
783	109	7.1	412	11	US-11-054-515-1865	Sequence 1865, Ap
784	109	7.1	640	9	US-11-054-515-1600	Sequence 1600, Ap
785	109	7.1	640	9	US-11-290-153-368	Sequence 368, App
786	109	7.1	640	9	US-11-299-153-368	Sequence 368, App
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790	109	7.1	771	11	US-11-147-047-34	Sequence 34, Appl
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806	108.5	7.0	258	9	US-11-266-444-1274	Sequence 1274, Ap
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819	108.5	7.0	934	11	US-11-046-653-4	Sequence 4, Appli
822	108.5	7.0	945	9	US-10-977-1115B-146	Sequence 146, App
823	108.5	7.0	945	11	US-11-183-136-18	Sequence 18, Appl
824	108.5	7.0	945	11	US-11-183-136-20	Sequence 20, Appl
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826	108	7.0	203	11	US-11-197-038-18	Sequence 18, Appl
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828	108	7.0	204	11	US-11-197-038-17	Sequence 17, Appl
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863	108	7.0	439	11	US-11-197-038-33	Sequence 33, Appl
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875	107.5	7.0	248	11	US-11-054-515-1816	Sequence 1816, Ap
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906	107.5	7.0	213	9	US-11-290-153-438	Sequence 438, Ap
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908	107	6.9	237	11	US-11-204-709-23	Sequence 23, Appl
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918	107	6.9	259	11	US-11-054-515-1034	Sequence 1034, Ap
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923	107	6.9	458	11	US-11-089-803-6	Sequence 6, Appli
924	107	6.9	458	11	US-11-149-738-2	Sequence 2, Appli
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926	107	6.9	458	11	US-11-193-746-2	Sequence 2, Appli
927	107	6.9	458	11	US-11-218-234-6	Sequence 6, Appli
928	107	6.9	458	11	US-11-218-234-8	Sequence 8, Appli
929	107	6.9	463	11	US-11-000-463-872	Sequence 872, App
930	107	6.9	463	9	US-10-463-872	Sequence 6, Appl
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974	106	6.9	309	9	US-10-453-372-778	Sequence 778, App
975	106	6.9	330	9	US-11-085-812-2	Sequence 2, Appl
976	106	6.9	434	11	US-11-204-709-24	Sequence 24, Appl
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982	106	6.9	446	11	US-11-102-621-123	Sequence 123, App
983	106	6.9	483	11	US-11-299-182-16	Sequence 16, Appl
984	106	6.9	525	11	US-11-236-198-13	Sequence 13, Appl
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1097	103.5	6.7	243	9	US-11-211-917-80	Sequence 80, Appl
1098	103.5	6.7	243	11	US-11-211-917-102	Sequence 102, App
1099	103.5	6.7	243	11	US-10-016-686-1	Sequence 1, Appli
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1103	103.5	6.7	245	9	US-10-115-609-2	Sequence 2, Appli
1104	103.5	6.7	245	11	US-11-054-515-1896	Sequence 1896, Ap
1105	103.5	6.7	247	11	US-11-266-444-1896	Sequence 1896, Ap
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1107	103.5	6.7	247	11	US-11-266-444-2092	Sequence 2092, Ap
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1109	103.5	6.7	248	11	US-11-266-444-1267	Sequence 1267, Ap

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1114	103.5	6.7	252	11	US-11-054-515-1557	Sequence 1557, Ap
1115	103.5	6.7	252	11	US-11-054-515-1646	Sequence 1646, Ap
1116	103.5	6.7	252	11	US-11-054-515-1698	Sequence 1698, Ap
1117	103.5	6.7	252	11	US-11-266-444-1557	Sequence 1557, Ap
1118	103.5	6.7	252	11	US-11-266-444-1646	Sequence 1646, Ap
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1125	103.5	6.7	334	11	US-11-113-424-80	Sequence 80, Appl
1126	103.5	6.7	416	9	US-10-453-372-1028	Sequence 1028, App
1127	103.5	6.7	431	11	US-11-198-819-14	Sequence 14, Appl
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1129	103.5	6.7	448	9	US-10-453-372-1024	Sequence 1024, App
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1132	103.5	6.7	456	9	US-10-453-372-1026	Sequence 1026, App
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1134	103.5	6.7	471	9	US-10-106-820-25	Sequence 25, Appl
1135	103.5	6.7	471	9	US-10-106-820-27	Sequence 27, Appl
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1137	103.5	6.7	471	11	US-11-190-364-23	Sequence 23, Appl
1138	103.5	6.7	471	9	US-11-147-780-22	Sequence 22, Appl
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1189	102.5	6.6	251	11	US-11-054-515-1149	Sequence 1149, Ap
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1256	101.5	6.6	251	11	US-11-266-444-894	Sequence 894, App
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1271	101.5	6.6	453	11	US-11-208-422-23	Sequence 23, Appl
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1273	101.5	6.6	462	11	US-11-177-648-28	Sequence 28, Appl
1274	101.5	6.6	462	11	US-11-177-648-92	Sequence 92, Appl
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1277	101.5	6.6	495	11	US-11-264-096-302	Sequence 302, Appli
1278	101.5	6.6	548	11	US-11-022-289-3	Sequence 3, Appli
1279	101.5	6.6	626	9	US-10-512-184-49	Sequence 49, Appl
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1297	101.5	6.6	253	11	US-11-190-364-18	Sequence 18, Appl
1298	101.5	6.6	253	11	US-11-147-780-18	Sequence 18, Appl
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1316	101.5	6.6	902	11	US-11-205-935-12	Sequence 12, Appl
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1318	101.5	6.6	902	11	US-11-205-935-14	Sequence 14, Appl
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1353	100.5	6.5	237	11	US-11-054-515-2118	Sequence 2118, Ap
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